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                      Copyright
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- protein search, using sw model OM protein

; Search time 218.87z seconds (without alignments)
1282.772 Million cell updates/sec Search time 218.872 Seconds February 28, 2006, 08:37:25 Run on:

US-10-717-665A-44 3349° -1 MPQPSVSGMDPPFGDAFRSH.....TAEGNPTGGLVGLRIPTSKV 639 Title: Perfect score:

BLOSUM62 Scoring table: Sequence:

2443163 seqs, 439378781 residues Gapop 10.0 , Gapext 0.5 Searched:

2443163 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* A_Geneseq 21:* Database

geneedp19908:* geneedp20008:* geneedp20018:* geneedp20018:* geneedp2003a8:* geneedp20038:* geneedp20048:* 4.0.00

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Adk65805 Angiogene	2 Novel	Ado20373 Human PRO	Adk35935 Novel hum	Abp64928 Human pro		Adk65836 Angiogene	Ade61623 Rat Prote	Add46090 Rat Prote	8 Rat	0	Abg29275 Novel hum		0	Aab62331 Amino aci	Каров		Adv68154 Kaposi's	Aae37016 Human nuc	Aaw01897 Nonsense-	Aay98056 Yeast NMD	Aaw01896 Nonsense-	5 Yeast	Aay98055 Yeast Nmd
ID	ADK65805	ADQ66472	AD020373	ADK35935	ABP64928	ABB68374	ADK65836	ADE61623	ADD46090	ADE57828	ADE57830	ABG29275	AAY96255	AAY58500	AAB62331	ABB05621	ADJ65096	ADV68154	AAE37016	AAW01897	AAY98056	AAW01896	AAY05835	AAY98055
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% Query Match Length	639	417	296	256	168	814	91	712	712	712	712	160	1162	1162	1162	1162	1162	1162	735	764	764	1089	1089	1089
% Query Match	100.0	64.1	45.8	37.9	25.8	15.1	13.0	6.0	6.0	9.0	0.9	6.0	5.9	5.9	5.9	5. 9.	5.9	5.9	5.7	5.5	5.5	5.5	S	5.5
Score	3349	2148	1534	1268	865	206	434	202	202	202	202	200.5	196.5	196.5	196.5	196.5	196.5	196.5	189.5	184	184	184	184	184
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	-	Aeb22174 Plasmodiu	Aam39101 Human pol	Human	Add01163 Human nuc	Abp96961 Human BMC	Human	Human	Human	Add46092 Human Pro	Aar79912 Human nuc	Human	Aab48964 Human nuc	Add49220 Human nuc		Adp54086 Human PRO	Ady19864 PRO polyp		Abg09944 Novel hum	Abm87025 Rice abio	
AAB85725	ABP73549	AEB22174	AAM39101	AAM40887	ADD01163	ABP96961	ADP46649	ADP46648	ADE61625	ADD46092	AAR79912	AAW84052	AAB48964	ADD49220	ADJ58974	ADP54086	ADY19864	ABM80398	ABG09944	ABM87025	
842 4	427 5	553 9	279 4	305 4	7 09 7	724 6	520 8	568 8	7 907	7 907	707 2	707 2	707 4	7 707	707 8	707 8	707	710 8	97 4	722 7	
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25	26	27	28	29	30	31	32	33	34	32	36	37	38	6	40	41	4	43	4 4	45	

ALIGNMENTS

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cytostatic; cardiant; vasotropic; antiarteriosclerotic; anglogenesis inhibitor; anglogenesis stimulator; anglogenesis stimulator; anglogenic index; gene expression; cancer; coronary artery disease; myocardial ischemia; coronary arteriosclerosis; forensic medicine.
                                                                     Angiogenesis-differentially expressed protein ANH0757.
                 ADK65805 standard; protein; 639 AA.
                                                                                                                                                                                                                   07-FEB-2002; 2002US-00067482.
10-JUN-2002; 2002US-00164595.
16-AUG-2002; 2002US-0403649P.
03-JAN-2003; 2003US-0437746P.
                                                                                                                                                                                                   07-FEB-2003; 2003WO-US003848
                                                     06-MAY-2004 (first entry)
                                                                                                                                                              WO2003066831-A2.
                                                                                                                                            Homo sapiens.
                                                                                                                                                                                14-AUG-2003.
                                    ADK65805;
RESULT 1
ADK65805
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(ORIG-) ORIGENE TECHNOLOGIES INC.

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Jay

Fan W,

Li X, Kovacs KF, WPI; 2003-731502/69. Sun Z,

N-PSDB; ADK65804.

Determining the angiogenic index of a tissue or cell sample using expression levels of differentially expressed genes, useful for diagnosing or treating cancer, coronary artery disease, myocardial ischemia and/or arteriosclerosis.

Claim 23; SEQ ID NO 44; 296pp; English.

The invention relates to a method of determining the anglogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the anglogenic index. The methods and compositions of the present

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The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% to 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a protein sequence of the invention.
                                                                                                 21-JAN-2003; 2003JP-00102206
09-MAY-2003; 2003JP-00131392
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invention are useful for diagnosing, preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary arteriosclerosis. They can also be used in research drug discovery and foransic medicine involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention.
                                                                                                                                                                                    MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL
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                                                                                                              100.0%; Score 3349; DB 7;
100.0%; Pred. No. 8.4e-248;
iive 0; Mismatches 0;
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Matches 639; Conservative
                                                                                     Sequence 639 AA;
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Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers

Claim 1; SEQ ID NO 3633; 2449pp; English

Length 417;

Sequence 417 AA;

ŝ Ishii

ľ Sato

Wakamatsu A,

Otsuki T,

Sugiyama T, Isono Y,

Yamamoto J,

Isogai T,

WPI; 2004-535376/52. N-PSDB; ADQ64284

Nagai K,

(REAS-) RES ASSOC BIOTECHNOLOGY

21-JAN-2004; 2004EP-00001196

EP1440981-A2

28-JUL-2004

Irie R;

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120
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                                                                  1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQONPFDFF
                                                                                                                                                             DDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSR
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                           Gaps
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                           Indels
Score 2148; DB 8;
Pred. No. 6.5e-156;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO20373 standard; protein; 296
 64.1%;
             Best Local Similarity 99.8 Matches 407; Conservative
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osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia;

Ното варіепв

cancer

Novel human protein sequence #1445

07-OCT-2004

ADQ66472;

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417

ADQ66472 standard; protein;

ADQ66472

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel PRO polypeptide e.g., PRO69614, PRO711106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for retacting and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, theumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic socierosis, sjograen's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating diseases of the Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy, polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                           rhemmatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
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                                                                               immune related disorder; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Schoenfeld J, Williams PM;
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                                                                                                                                            diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
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Pred. No. 5.1e-109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; SEQ ID NO 1266; 1731pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                  Chiu H,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.8%;
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                                                                                                                                                                                                                                                                                                                                                                    08-NOV-2002; 2002US-0425235P
                                              Human PRO polypeptide #633
             (first entry)
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Matches 294; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spondyloarthropathy.
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N-PSDB; ADO20372.
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Wu TD;
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                                                                                                                                                                                                                                Homo sapiens.
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Wood WI,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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nucleotide sequence selected from one of 1680 sequences, a mature protein coding portion of them, an active domain of them and their complementary sequences. The invention may be useful for the production of compounds with an antiarthritic, antiparkinsonian, neuroprotective, nootropic, immunosuppressive, cytostatic, antiparatic, antiparasitic activity. In addition, the disclosed sequences may be useful for gene therapy. The polypeptides or their antibodies are useful for treating many diseases such as arthritis, parkinson's, Alzheimer's autoimmune diseases, cancer, psoriasis, inflammatory bowel disease and infections caused by bacteria, viruses, fungi or parasites. The present sequence is that of a human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polynuclectide encoding bone marrow derived polypeptides useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's disease, and inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .256
/label= OTHER
/note= "OTHER= All Xaa's in this sequence are unknown
amino acids or the site of a stop codon within the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel isolated polynucleotide comprising a
584 ERGENMGOKLBILIKDTLGLPVAGOTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 639
241 ERGENMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                            antiarthritic; antiparkinsonian; neuroprotective; nootropic; immunosuppressive; cytostatic; antipsoriatic; antiinflammatory; santibacterial; antiviral; antifungal; antiparasitic; gene therapy; arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer; psoriasis; inflammatory bowel disease; infection; bacteria; virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.9%; Score 1268; DB 5;
98.8%; Pred. No. 1.1e-88;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      claim 20; SEQ ID NO 8017; 504pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                           Š
                                                                                                                                                                                                                               Novel human polypeptide SeqID8017.
                                                                                                                           ADK35935 standard, protein; 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAR-2001; 2001WO-US004941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2000; 2000US-00519705.
19-MAY-2000; 2000US-00574454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 98.8
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence"
                                                                                                                                                                                                                                                                                                                                                      fungus; parasite; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-280918/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 256
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2002
                                                                                                                                                               ADK35935;
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                                                                                            RESULT 4
                                                                                                            ADK35935
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Disclosure; SEQ ID NO 31914; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB68374 standard; protein; 814 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                        Query Match 25.8°
Best Local Similarity 100.
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                        Sequence 168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABL12477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB68374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
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                                                                    282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        central nervous system disease, viral infection;
certral nervous system disease, non-healing wound; infectious disease;
limmune deficiency; immune disorder; non-healing mound; allergy; cancer;
fungal infection; autoimmune disorder; coaquiation disorder; nootropic;
antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
cytostatic; haemostatic; virucide; antibacterial; fungicide;
immunostimulant; cerebroprotective.
                                                                                       EKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPL 124
                                                                                                                                                                402
                               64
                                                                                                                                                                                                                                   Zhao QA;
                             5 VKQNPLPSSFPGKKITIRLAAPVCSSKTLQAEVPLSDCVQKASKPTSSTQIMVKTNMYHN
                                                                                                                                         QCHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVS
                                                                                                                                                                                                              DNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHELSENEEEEEEEEDYEDDKDDDISD
                                                                    EKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; expressed sequence tag; EST; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Goodrich RW, Liu C, Zhou P, Asundi V,
Xue AJ, Yang Y, Wehrman T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 588; 394pp; English
                                                                                                                                                                                                                                                                                                                                                                                                              ABP64928 standard; protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-2001; 2001WO-US042950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein SEQ ID 588.
                                                                                                                                                                                                                                                                                       TFSEPG 408
                                                                                                                                                                                                                                                                                                                     245 TPSEPG 250
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Ren F, X
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                                                                    223
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ABP64928 RESULT

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cc nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or pluripotential state conseful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaccuticals or the development of bio-sensors. The colloporating disorders are useful for preventing, treating or amaliorating disorders involving aberrant protein expression or biological activity, e.g. haematopoietic disorders, central/peripheral corrections system diseases, mechanical and traumatic disorders, non-healing wounds, immune deficiencies and disorders, infectious diseases caused by viral, bacterial or fungal infection, autoimmune disorders, non-healing corrections and conditions, coagulation disorders, or cancer. The polymucleotide sequences of the invention were assembled from ESTs isolated mainly by sequencing by hybridisation, and in some cases, captances obtained from one or more public databases. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 QEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 MVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 QEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 EHNYSLFVSDNLGEQPTKCSPEDDEDDEDVDDEDHDEGFGSEH 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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100.0%; Pred. No. 4.9e-58;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EM.
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ADK65836 standard; protein; 91 AA

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25;
           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57137-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               732
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                                                                                                                                                                                                                                                                                                                                                                    257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---ISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKONPLPSSF-PGKKITSRAAAPVCSS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 VQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----QSAALSPGG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 QEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----EEEEEDY 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LGLEHIWMRREPRQHLLSTGSLAEAESFSSLSTGSVLSPDGIDFSQDDEDDN 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 EDDKODDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQERML-- 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLL 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------ YQDEEV-- 132
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                                                                                                                                                                                                                                                                                                                                                        205 SSNGIGSGSGGGYFTPDMSHSLSLNVVSEQVLLQBATTFN-----BLLYEMTPNSNAMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 SSGFGSSASGNSTTTSNQTS---GSAVRKSFGYQSAVENSQLSRLSSSAPTH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---IEDFLPQTAV-----TQSVNFLLSPQAQGQDALVAPPMELLQQQQQNHQQLQVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 KTLQAEVPLSDCVQKASKPPSST----QIMVKTNMYHNEKVNFHVECKDYVKKAKVKINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
15.1%; Score 506; DB 4; Length 814;
Best Local Similarity 25.0%; Pred. No. 1.7e-29;
Matches 186; Conservative 94; Mismatches 211; Indels 254; Gaps
                                                                                                                                                                                                                                                                                                                               SVSGMDPPFGDAF---RSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL-
                                                                                                                                                                                                                                                                                                                                                                                                                                           258 SDISSAIIHTKHEPFSLDDDYIFPNDKAEIQAADLSDLNGGDFLDVIGN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 LPQLQTLLTLSQQQQSNSSSTSPYEIYHSTPQXPQQQQLSASFSPGSQASQSPLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 DTYCEDLIKYTKLISCDIWGTKEVDYL-----GLDDFSSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSEFVNQVLEKTAEGNPTGGLVGLR 633
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                                                                                                                                                                                                                       Sequence 814 AA;
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ADK65836 RESULT

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a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the angiogenic index. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary arteriosclerosis. They can also be used in research, drug discovery and forensic medicine involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention.
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                                                                                                                             angiogenesis inhibitor; angiogenesis stimulator; angiogenic index; gene expression; cancer; coronary artery disease; myocardial ischemia; coronary arteriosclerosis; forensic medicine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining the angiogenic index of a tissue or cell sample using expression levels of differentially expressed genes, useful for diagnosing or treating cancer, coronary artery disease, myocardial ischemia and/or arteriosclerosis.
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                                                                                                                    cardiant; vasotropic; antiarteriosclerotic;
                                                                                    Angiogenesis-differentially expressed protein #50
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100.0%; Pred. No.....
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                             Jay
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                                                                                                                                                                                                                                                                                                                  07-FEB-2002; 2002US-00067482.
10-JUN-2002; 2002US-00164595.
16-AUG-2002; 2002US-0403649P.
03-JAN-2003; 2003US-0437746F.
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                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 91 AA;
                                                                                                                                                                                                  Homo sapiens
                                                          06-MAY-2004
                                                                                                                     cytostatic;
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                                 Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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22.4%; Pred. No. 3.1e-06;
Live 60; Mismatches 171; Indels 140;
                                                                                                                                                                                                                                                                                                                                                               Costigan M;
Rat Protein P13383, SEQ ID NO 7544
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                                                                                                                                                                                                                                                                                                                                                               Befort K,
                                                                                                                                                                                                                                   14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                 14-AUG-2002; 2002WO-US025765.
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GENBANK; P13383.
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                                                                                          Rattus norvegicus
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or human polynucleotides or applynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also comprising the rovel polynucleotide, a host cell comprising the vector comprising the novel polynucleotide, a host cell comprising the vector, amethod for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially
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                                                                                                                                                                        GKNAKKEDSDEDEDEDEDDSDEDEDEDEREPPVVKGVKPAKAAPAAPASEDEDDD
                                                                                                                                                                                                                                               363 DVDDEDHDEGFGSEHELSENEEE-------EEEEEDYEDDKDD
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Costigan M;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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14-AUG-2002; 2002WO-US025765.

27-FEB-2003

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expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or thair antibodies. The polynucleotide or the compound that colympeptides or thair antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (CMI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at [tp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity 22.4%; Pred. No. 3.1e-06;
Matches 107; Conservative 60; Mismatches 171; Indels 140; Gaps
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Matches 107; Conservative
Best Local Similarity
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                                                                                                                                                                                                                            Rat Protein AAA41732, SEQ ID NO 3693
                                                                                                                  ADE57828 standard; protein; 712
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                                                                                                                                                                                                                                                                                                                        Rattus norvegicus.
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29-JAN-2004

ADE57828

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The invention discloses a composition to more insurance of the invention discloses a composition of the nucleic acid sequence. Also derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymuclectide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a composition of a polymucleotide sequence that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which regulates the activity of one or more of the composition, a compound that regulates the activity of one or more of the composition, a method for identifying a compound second that regulates the activity of one or more of the polymetication a method for identifying a compound second that regulates the activity of one or more of the polymetication a method for identifying a compound second that regulates the activity of one or more of the polymetication and appendix a method for identifying a compound second that regulates the compound second that regulates the activity in an animal of one or more of the polymetical composition or more of the polymetical composition comprising the one or more polymetical second injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene injury (CLI) and spared nerve injury (SNI) in an animal (e.g. gene the sequence presented is a rat protein (shown in Table 2 of the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed specification) which is differentially expressed during pain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 KTLOAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS
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                                                                                                                                                                                                                                                                                   Befort K,
                                                                                            14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
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                                                                                                                                                                                                                                                                                                                                  WPI; 2003-268312/26
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or human polymucleotides or a polymucleotide which represents a fragment, calaimed are a vector comprising the movel polymucleotide, a host cell comprising the vector comprising the movel polymucleotide, a host cell comprising the vector comprising the movel polymucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pactivity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition compressing the or more or mor
                                                     DISDIFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQ--ERMLRPSEWN 456
                                                                                                                                                               457 RDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVS 516
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DEDDDDDDE---EEEEEDDSEEEVMEITPAKGKKTPAKVVPVKAKSVAEEEEDDEDDEDE 252
                                                                                                       EEDE--DEEDEEDEDEDEEEEEEPVKAAPGKRK-----KEMTKQKEAPEAKKQKIEGS 304
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                                                                                                                                                                                                                                                                                                        two or more isolated polypeptides, useful treating pain in an animal.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
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pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            517 EL-PLTARPRSRKEKNKLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQE 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 GKNAKKEDSDEDEDEDEDEDEDEDEDEFEPPVVKGVKPAKAAPAAPASEDEDEDD
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                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                6.0%; Score 202; DB 7; Length 712;
22.4%; Pred. No. 3.1e-06;
tive 60; Mismatches 171; Indels 140;
                                                                                                           frp.wipo.int/pub/published_pct_sequences.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                Sequence 712 AA;
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The present sequence is the Kaposi's sarcoma-associated herpesvirus, CC (KSHV) latency-associated nuclear antigen (LANA). KSHV is also known as Human Herpes Virus 8 (HHV8) and belongs to the rhadino virus, or gamma-2 herpes virus class. The LANA protein is necessary for the efficient persistence of rhadino virus DNA in mammalian cells. Persistent rhadino virus infection is implicated in a variety of diseases e.g. Kaposi's Sarcoman (KS). Primary Effusion Lymphona (PEL) and multicentric castlemen's disease. In addition, KS is a common malignancy in HIV patients. KSHV persists in host cells in a latent form. One of the few genes expressed from the latent viral DNA is LANA. Associates with coth human chromosomes and with the rhadino virus cis-acting element (RVCAE), thereby providing a tethering function: the KSHV DNA episome is "tied" to the host chromosomes. This allows the viral DNA to persist in the host cell. The present sequence may be used to screen and identify molecules that inhibit LANA interaction with RVCAE, thereby interfering with the latency cycle of this virus. Potential antiviral treatments for the above mentioned diseases may therefore be based on LANA deregulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 PVCSSKTLOAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating or preventing a disease associated with rhodino virus infection in a mammal which includes Kaposi's Sarcoma and Primary Effusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.9%; Score 196.5; DB 3; Length 1162;
24.2%; Pred. No. 1.7e-05;
tive 52; Mismatches 145; Indels 103;
                                                                         550. .589
/note= "Gln, Glu, Pro, Arg-rich region"
590. .759
/note= "Gln, Glu, Asp-rich region"
760. .840
                                                       "Gln, Glu, Pro-rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                         /note= "Gln, Glu-rich region"
                     note= "acidic repeat region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaye KM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 7; 70pp; English
                                                                                                                                                                                                                                                                                                                             98US-00109422
99US-00298568
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/note= "م"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kieff ED, Ballestas ME,
                                                                                                                                                                                                                                                                                                                                                                                                     (BALL/) BALLESTAS M E. (KAYE/) KAYE K M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-387829/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                             WO200029626-A1
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                                                                                                                                                                                                                                                                                         19-NOV-1999;
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21-APR-1999;
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                                                                                                                                                                                                                           The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed construction of (II). The polymucleotides are also used in diagnostics as useful in gene therapy techniques to resore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a colypoptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders convolving aberrant protein expression or biological activity. The colypoptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540 LKKKAQYEANKVKLW-GLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIK 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus; latency-associated nuclear antigen; LANA; gamma-2 herpes virus; Human herpes virus element; RVCAE; Kaposi's sarcoma; primary effusion lymphoma; PEL; human immunodeficiency virus; HIV; multicentric Castleman's disease.
                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14. .17
/note= "nuclear localisation signal, NLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "nuclear localisation signal, NLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%; Score 200.5; DB 4; 73.0%; Pred. No. 4.4e-07; tive 2; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaposi's sarcoma-associated herpesvirus LANA.
                                                                                                                                                                                               Claim 20; SEQ ID NO 59634; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 73.09
Matches 46; Conservative
                                         WPI; 2001-639362/73
       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            599 DTL 601
                                                               N-PSDB; AAS93462
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                                                                                                                                                             biodiversity.
       Drmanac RT,
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human herpes virus type 8 (HHV8, a gammaherpeavirus) HHV8 plays an human herpes virus type 8 (HHV8, a gammaherpeavirus) HHV8 plays an human herpes virus type 8 (HHV8, a gammaherpeavirus) HHV8 plays an important role in the pathogenesis of AIDS-related Kaposi's sarcoma. The invention relates to a novel method of detecting the presence of human herpesvirus 8 in a biological sample using peptides representative of cominant antigonic regions of HHV8. The method comprises contacting one or more isolated, immunogenic HHV8 peptides with an antibody-containing biological sample, and detecting the formation of a complex between the presence of human herpesvirus 8. The detection of HHV8 infection can be used to diagnose AIDS-associated Kaposi's sarcoma. The HHV8-specific antibodies are useful therapeutically when for the passive immunisation of a human against HHV8 infection, thereby reducing HHV8 related disease. The detection assays are highly specific, sensitive accurate Early detection assays are highly specific, sensitive cacurater Early detection and treatment of Kaposi's sarcoma could diminish the severity of symptoms related to AIDS and the sensitive centiques could reduce erroneous characterisations of skin disorders. Evering assays for HHV8 antibodies such as immunoblots and enzyme immunosassays lack the sensitivity and accuracy meded for reliable diagnosis of Kaposi's sarcoma. Further advantages of
SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
                                                        ----- 368
                                                                                            369 HDEGFGSEHELSENEEEEEEEDYEDDKODDISOTFSEPGYENDSVEDLKE----- 419
                                                                                                                                                              380 DDEEDDEEDDEEDDEEDDEEDDEEDDEDDDEDNEDE-----EDDEEEDKKEDEEDGGDGN 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHV8; detection; diagnosis; Kaposi's sarcoma; AIDS; immunogen; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New methods and compositions for the detection of human herpesvirus
                                                                                                                                                                                                                                     420 -VTSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSE 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                        NYSLFVSDNLGEQPTKCSPEEDEEDEE-
                                                                                                                                                                                                                                                                                                                                                    AAY58500 standard; protein; 1162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 59-62; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HHV8 ORF 73 protein, SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US011407.
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                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human herpesvirus 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-097142/08
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10-APR-2000
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                                                                                                                                                                                                                                                                                                               RESULT 14
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                                                                                                                                                                                                                                                              208
                                                                                                                                                                                                                                                                                                                              268
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   18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis; Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8; KSHV; latency-associated nuclear antigen; LANA.
                                                                                                                                                                124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA
                                                                                                                                                                                              111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR
                                                                                                                                                                                                                                                            163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PQ
                                                                                                                                                                                                                                                                                              238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH
                                                                                                                                                                                                                                                                                                                         209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS
                                                                                                                                                                                                                                                                                                                                                            286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH
                                                                                                                                                                                                                                                                                                                                                                                           269 SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNOAGED---NGDNEISKESQVDKDD
                                                                                                                                                                                                                                                                                                                                                                                                                              --- DVDDED
                                                                                                                                                                                                                                                                                                                                                                                                                                               380 DDEEDDEEEDEEEDEEEDEEEDDEEDDDDEDNEDE-----EDDEEDDKKEDEEDGGDGN
                                                                                                                                                                                                                              184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK
                                                                                                                                 Gaps
   method
the assays are that reproducible results are obtained and the method suitable for rapid throughput and screening of samples economically. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                              Query Match 5.9%; Score 196.5; DB 3; Length 1162; Best Local Similarity 24.2%; Pred. No. 1.7e-05; Matches 96; Conservative 52; Mismatches 145; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 HDEGFGSEHELSENEEEEEEDYEDDKDDISDTFSEPGYENDSVEDLKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of KSHV tethering protein LANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420 -VTSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSE 454
                                                                                                                                                                                                                                                                                                                                                                                                                              336 NYSLFVSDNLGEQPTKCSPEEDEEDEE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB62331 standard; protein; 1162 AA
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N-PSDB; AAF82901.
                                                                   Sequence 1162 AA;
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29-JUN-2001
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protein and expression vector operationally encoding a protein autiable for tethering the nucleic acid to the histone H1 protein, where the tethering protein is LANA. The composition is useful in aiding the retenting protein is LANA. The composition is useful in aiding the cremation of the viral DNA in the host cell. The viral vector encodes a protein suitable for tethering DNA to Histone H1. Methods for screening for compounds which are agonistic or antagonistic for the tethering of viral proteins to histone H1 and DNA binding sites are useful for developing the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis, Parkinson's disease, Huntington disease and diabetes. The present sequence represents the amino acid sequence of the Kaposi's sarcoma associated herpesvirus (human herpesvirus 8) latency-associated nuclear antigen (LANA), which acts as a tethering protein. (Updated on 06-AUG-2003 to correct OS field.)
                                                                              acid, histone
                                                                              The invention provides a composition comprising nucleic
                     Disclosure; Fig 9B; 60pp; English
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Sequence 1162 AA;

14; 184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237 238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285 10 GPSTINPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS 268 286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335 269 SSPSEGSWGDDTAMLVILAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325 336 NYSLFVSDNLGEQPTKCSPEEDEEDEE -----------------------------DVDDED 368 369 HDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE------ 419 124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKONPLPSSFPGKKITSRAAA 183 Query Match
5.9%; Score 196.5; DB 4; Length 1162;
Best Local Similarity 24.2%; Pred. No. 1.7e-05;
Matches 96; Conservative 52; Mismatches 145; Indels 103; Gaps 420 -VTSISSRKRGKRRYFWEYSEQLTPSQOERMLRPSE 454 요 g ð g Š g ઠે 셤 ઠે g ઠે 8 ઠ

Search completed: February 28, 2006, 08:45:04 Job time: 222.872 secs

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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                      Copyright
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OM protein - protein search, using sw model

February 28, 2006, 08:53:26; Search time 54.985 Seconds Run on:

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960.804 Million cell updates/sec

US-10-717-665A-44 3349 1 MPQPSVSGMDPPFGDAFRSH......TAEGNPTGGLVGLRIPTSKV Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Sequence:

Scoring table:

572060 segs, 82675679 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:* Issued_Patents_AA: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de				
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
-	3349	100.0	639	2	US-10-164-595-44	Sequence 44, Appl
8	434	13.0		~	US-10-164-595-75	
m	324	9.7		~	US-09-270-767-41799	417
4	324		141	~	US-09-270-767-57041	
S	196.5		1162	Н	US-08-728-323A-2	7
9	196.5	5.9	1162	~	US-09-298-568-2	7
7	196.5	5.0	1162	~	US-09-410-399-2	7,
œ	196.5	5.9	1162	~	US-09-894-273-2	ď
6	184	5.5	764	Н	US-08-375-300-4	4,
10	184	5.5	764	~	US-09-177-431-4	4
11	184	5.5	764	4	PCT-US95-16930-4	4,
12	184	5.5	1089	н	US-08-375-300-2	~
13	184	5.5	1089	~	US-09-177-431-2	7
14	184	5.5	1089	4	PCT-US95-16930-2	Sequence 2, Appli
15	176.5	5.3	428	7	US-09-248-796A-15197	15197
16	174	5.2	706	~	US-09-538-092-957	
17	174	5.2	747	7	US-09-949-016-10040	10040
18	170.5	5.1	311	~	US-09-902-540-10544	Sequence 10544, A
19	170.5	5.1	1231	~	US-08-714-741-41	Sequence 41, Appl
20	166.5	5.0	412	~	US-08-741-134-2	7
21	166.5	5.0	542	~	US-08-935-855-22	
22	166.5	5.0	709	7	US-09-248-796A-19045	Seguence 19045, A
23	164.5	4.9	687	~	US-10-104-047-2651	Sequence 2651, Ap
24	164.5	4.9	1102	7	US-09-949-016-8427	Sequence 8427, Ap
25	163.5	4.9	1972	~	US-09-418-710-21	21,
56	163.5	4.9	1972	N	US-09-839-479-21	21,
27	162.5	4.9	714	Н	US-08-990-114-3	ω,

Sequence 3, Appli Sequence 20628, A	Seguence 4, Appli Seguence 9676, Ap	Sequence 72, Appl Sequence 71, Appl	Sequence 2, Appli Sequence 2, Appli		2449	28,	Sequence 28, Appl	Sequence 28, Appl	Sequence 20, Appl	Sequence 827, App	Sequence 6265, Ap	Sequence 7397, Ap	Sequence 10326, A
US-09-241-333-3 US-09-248-796A-20628	US-09-047-026A-4 US-09-949-016-9676	US-09-418-710-72 US-09-839-479-71	US-08-822-701-2 US-08-935-855-2	US-09-248-796A-16660	US-09-248-796A-24492	US-08-431-080-28	US-08-938-534-28	US-09-345-294-28	US-08-935-855-20	US-09-538-092-827	US-09-949-016-6265	US-09-949-016-7397	US-09-949-016-10326
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ALIGNMENTS

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61 SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL 120
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                                                                APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis of
FILS REPERBNCE: 10 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
            Sequence 44, Application US/10164595
Patent No. 6657054
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 639; Conservative
                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-164-595-44
US-10-164-595-44
                                                                                                                                                                                        SEQ ID NO 44
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558 TEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLE---
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APPLICATION NUMBER: US/08/728,323
                                                                                                                                                                                                                                                Sequence 57041, Application US/09270767 Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       610 SEFVNQVLEKTAEGNPTGGLVGLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Drosophila melanogaster US-09-270-767-57041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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: U.S.A.
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US-09-270-767-57041
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LENGTH: 141
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COUNTRY:
ZIP: 1003
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                                                                                                         481 RRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVSELPLTARPRSRKEKNKLAFRACRL 540
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Sequence 41799, Application US/09270767

Parent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 41799

LENGTH: 141
TSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKS
                                  421 TSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKS
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APPLICANT: Origene Technologies, Inc
APPLICANT: Origene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REPERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 75
LENGTH: 91
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49.3%; Pred. No. 5.2e-20;
iive 22; Mismatches 37; Indels
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Patent No. 6657054
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ORGANISM: Drosophila melanogaster
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Matches 71; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 83; Conserv
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US-10-164-595-75
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                                               61 IEHKRIMNGIAELKQALVVK-----HRTKNLGESTEEVDQQIARIYATASSGIRIAGGS 114
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE PERERRNCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN OF: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 14; Gaps
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APPLICANT: Bohenzky, Roy A.
APPLICANT: Busso, James J.
APPLICANT: Bedlan, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA TITLE OF INVENTION: Encoding Same And Uses Thereof NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
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9.7%; Score 324; DB 2; L
Best Local Similarity 49.3%; Pred. No. 5.2e-20;
Matches 71; Conservative 22; Mismatches 37;
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1185 Avenue of the Americas
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Query Match
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APPLICANT: Kieff, Elliott D.
APPLICANT: Rajestes, Mary B.
APPLICANT: Rajestes, Mary B.
APPLICANT: Rajestes, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT PELLING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
SOFTWARE: PAGENTIN Ver: 2.0
SOFTWARE: PAGENTIN Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK
                                                                                                                                                                                                                                                                                                                                                                  Indels 103; Gaps
                                                                                                                                                                                                                                                                                                                               Length 1162;
PILING DATE:
CLASSIFICATION: 435
ATTORNSIVE CANTION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPERRENCE JOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-391-0525
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: mino acid
TYPE: mino acid
                                                                                                                                                                                                                                                                                                                            5.9%; Score 196.5; DB 1; 24.2%; Pred. No. 1.2e-07; trive 52; Mismatches 145;
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; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-2
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US-09-298-568-2
; Sequence 2, Application US/09298568
; Patent No. 6322792
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 24.2*
Matches 96; Conservative
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APPLICANT: Robertson, Erle S.
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PAtentIn Ver. 2.0
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                                                                                                                                                         111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 SSPSEGSWGDDTAMLVILAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
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                                                                                                                                                                                                                                                                       209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS
                                                                                                                 124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA
                                                                                                                                                                                                                                      PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK
                                                                                                                                                                                                                                                                                                                                                       238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH
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5.9%; Score 196.5; DB 2; Length 1162;
24.2%; Pred. No. 1.2e-07;
ative 52; Mismatches 145; Indels 103;
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; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 NYSLFVSDNLGEOPTKCSPEEDEEDEE---
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                                                                96; Conservative
                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1162
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                                    Best Local
Matches 9
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Indels
                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
5.5%; Score 184; DB 1; L
Best Local Similarity 20.2%; Pred. No. 7.4e-07;
Matches 98; Conservative 69; Mismatches 159;
                                                                                                                                                                                                                                                                                                                NAME: Fasse, J. P.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046001
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
TELEPRAX: (617)542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 764 amino acids
amino acid
                                                                                                            STREET: 225 Franklin Strate: Boston STATE: MA COUNTRY: USA ZIP: 02110-2804 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
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--DVDDED 368
                  -----PQ 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
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                                                         369 HDEGFGSEHELSENEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE
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5 SOFTWARE: Patentin Ver. 2.0
5 LENGTH: 1162
7 TYPE: PRT
7 ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-894-273-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYSLFVSDNLGEQPTKCSPEEDEEDEE-----
NYSLFVSDNLGEQPTKCSPEEDEEDEE-
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APPLICANT: Feng, He
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN
TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED mRNA DECAY FUNCTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 ISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQ-----NPLPSSFPGK-KITSRAAA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEED
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Qy 418 KEVTSISSRKRGKRRYFWBYSEQLTPSQOERMLRPSEWNRDTLPSNMYQKNGLHHGKYAV 477 Db 622RLLSDEB C2	SULT 11 T-195-16930-4 SEQUENCE 4, Applica GENERAL INFORMATIC TITLE OF INVENTITITLE OF INVENTITIE OF INVENTITITLE OF INVENTITIE OF INVENTITIES OF IN	COMPUTER READABLE FORM: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC compatible CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/16930 FILING DATE: 27-DEC-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/375,300 FILING DATE: 20-JAN-1995 ATTORNEY/AGENT INFORMATION: NAME: Passe, J Peter REGISTRATION NUMBER: 32,983 REFERENCE/DOCKET NUMBER: 04020/046WO1	Score 184; DB	133 ISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQ 133 ISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQ 1382 INNQPNPFYLNYSDPPDNYFRIQLVTTILL 184 PVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKT
Oy 556 LNTEYD 561 Db 759 LKRSFD 764 RESULT 10 US-09-177-431-4 ; Sequence 4, Application US/09177431 ; PAPLICANT: He, Feng ; APPLICANT: He, Feng ; APPLICANT: He, Feng ; APPLICANT: He, Feng ; TANDAMION: HE FENG	TITLE OF INVENTION: HETEROLOGOUS FOLIFFETIES FROUGLION IN TITLE OF INVENTION: HETEROLOGOUS FOLIFFETIES TROUGHTON INVESTED TO STREET SQUENCES: 18 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston STATE: MA COUNTRY: USA ZITE: 02110-2804 COMPUTER: EADABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible COMPUTER: IBM Compatible COMPUTER: IBM Compatible COMPUTER: TO NISHER: Windows 95 SOFTWARE: FASTEM: Windows 95 SOFTWARE: FASTEM: Windows 197 SOFTWARE: FASTEM: Windows 197 FILING DATE: PRICK APPLICATION DATA: PRICK APPLICATION NUMBER: 08/955,472 FILING DATE:	ATTORNEY/AGENT INFORMATION: NAME: Fases, J. Peter REGISTRATION NUMBER: 07917/050001 REFERENCE/DOCKET NUMBER: 07917/050001 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070 TELEFAX: 617/542-9806 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 764 amino acids TYPE: amino acid TOPOLOGY: Innear MOLECULE TYPE: peptide US-09-177-431-4	Query Match 5.5%; Score 184; DB 2; Length 764; Best Local Similarity 20.2%; Pred. No. 7.48-07; Matches 98; Conservative 69; Mismatches 159; Indels 160; Gaps 18; Qy 133 ISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGK-KITSRAAA 183 Db 382 INNQPNPFYLNYSDPPDNYFRIQLYTTILLNINKTPAAFTKKCKLLER 429 Qy 184 PVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNWYNNEKVNFHVBCKDYVKK 237 Db 430 -FFEYYFFIKEQPLPKETEFRVSSTFKKYSNIFGNTKFER 468 Qy 238 AKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQE 297	1

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5.5%; Score 184; DB 1; L 20.2%; Pred. No. 1.3e-06; tive 69; Mismatches 159;
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/050001
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STREET: 225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-177-431-2; Sequence 2. Application US/09177431; Patent No. 6071700; GENERAL INFORMATION:
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Query Match
Best Local Similarity 20.2%
Matches 98; Conservative
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STREET: 22.
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STATE:
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Sequence 2, Application US/08375300
Sequence 2, Application US/08375300
Seneral Information:
APPLICANT: Seng, He
APPLICANT: Beng, He
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN
TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED mRNA DECAY FUNCTION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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     -----FER 468
                                       238 AKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQE 297
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                                                                                                                                                                                                418 KEVTSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAV 477
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     430 -FFEYYTFIKEQPL------PKETEFRVSSTFKKYENIFGNTK-
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-8906
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APPLICATION NUMBER: US/08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: not rel
TOPOLOGY: linear
MOLECULE TYPE: protein
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TELEX: 2
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APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MENA DECAY FUNCTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                               707 INNOPNPFYLNYSDP-----PDNYFRIOLVTTILLNINRTPAAFTKKCKLLLR---
                                                                                                                                                                                                                                                 755 -FPEYYTFIKEQPL------PKETEFRVSSTFKKYENIFGNTK------FER
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                                                   Indels 160;
Length 1089;
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
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|024 KETYEELSKPKKIAFTFLTKSGKKTQSRILQLPTDVKFVSDVLEEEBKLKTERNKIKKIV 1083
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                                                                                                                                                                                                                          Query Match
5.5%; Score 184; DB 2; Length 1089;
Best Local Similarity 20.2%; Pred. No. 1.3e-06;
Matches 98; Conservative 69; Mismatches 159; Indels 160; Gaps
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GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE
TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF
TITLE OF INVENTION: PUNCTION FUNCTION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       947 ------RDIEMKRMYEEY------ERKLKDEE---
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225 Franklin Street Suite 3100
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-9806
                   TELEPHONE: 617/542-5070
TELEFAX: 617/542-9806
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
                                                                                                                                                                   , MOLECULE TYPE: protein US-09-177-431-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1084 LKRSFD 1089
                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
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02110-2804
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Sequence 15197, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1024 KETYBELSKPKKIAFTFLTKSGKKTQSKILQLPTDVKFVSDVLEEEEKLKTERNKIKKIV 1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1089;
                  PatentIn Release #1.0, Version #1.30
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Best Local Similarity 20.2%; Pred. No. 1.3e-06;
Matches 98; Conservative 69; Mismatches 159;
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                                                                                                                                                                                                                                                                                 04020/046WO1
                                     SOFTWAKE: FOREMLIN RELEGISE #1.0, VEES CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16930
FILING DATE: 27-DEC-1995
FILING DATE: 27-DEC-1995
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FASSE, J. PETER
REGISTRATION NUMBER: 32,983
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 32,983
REPERENCE/DOCKET NUMBER: 32,983
TELEPHONE: (617)542-5070
TELEPHONE: (617)542-5070
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amin-
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                                                                                                                                                                                                                                                                            Query Match 5.3%; Score 176.5; DB 2; Length 428;
Best Local Similarity 21.7%; Pred. No. 1.4e-06;
Matches 103; Conservative 71; Mismatches 152; Indels 149; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 --KSNTKKDDDDYQSEVLSKKEQRRLKKLQ-----TKQQEE------
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                                                                                                                                                                                                                                                                          Length 428;
     FOR DIAGNOSTICS AND THERAPEUTICS
FILLE OF INVENTION: FOR DIAGNOSTICS AND THER FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15197
LENGTH: 428
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                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15197
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Search completed: February 28, 2006, 08:56:05 Job time : 56.235 secs

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361 BEDVDDEDHDEGFGSEHELSENEEEEEEEDYEDDXDDDISDTFSEFGYENDSVEDLKEV 420
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Sequence 31914, A
Sequence 75, Appl
                                                                                           February 28, 2006, 08:54:36; Search time 186.308 Seconds (without alignments) 1433.071 Million cell updates/sec
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3349
1 MPQPSVSGMDPPFGDAFRSH.....TAEGNPTGGLVGLRIPTSKV
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-11-097-143-31914
US-10-717-665-75
US-10-450-763-59634
US-09-894-273-2
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US-10-450-763-40303
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US-10-487-593-1
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US-11-097-143-29151
US-10-104-047-2651
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US-10-425-114-58474
                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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US-10-384-569-3
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US-10-194-046-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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7, Appli 38, Appl 31, Appl 21, Appl 21, Appl 17, Appl 17, Appl 35, Appl 335, Appl 315, Appl 315, Appl 115765, Appl 115765, Appl 12765, Appl 17, Appl 17, Appl 17, Appl			Gaps	RDNFL RDNFL	DYLGL	SFPGKKITSR SFPGKKITSR	TKKAKV TKKAKV	PKETQELLL FKETQELLL	PEEDEED PEEDEED	DLKEV
Sequence Seq		Polypeptides	Length 639; Indels 0;	FMYELDREMNYQQNPRDNFL 	TSCDIWGTKEN	CONPLPSSFPGK 	CONFHUECKDYA	SHATPALPFKET SHATPALPFKET	OPTKCS 	GYENDS
US-11-013-684-7 US-10-369-493-22462 US-10-451-467A-388 US-10-376-537-21 US-10-376-537-21 US-10-756-148-21 US-10-756-149-5621 US-10-786-149-5621 US-10-732-923-332 US-10-732-923-332 US-10-732-923-313 US-10-732-923-313 US-10-732-923-313 US-10-732-923-311 US-10-732-923-311 US-10-702-143-15765 US-10-702-143-15765 US-10-376-537-72 US-10-376-537-72	ALIGNMENTS	enesis Genes and 7,665 595	Score 3349; DB 5; Lengt Pred. No. 3.1e-211; 0; Mismatches 0; Indel	SEQTLMSTDLLANSSDPD 	SLEDCKDIENLESFTDVLDNEGALTSNWEGWDTYCEDLTKYTKLTSCDIMGTKEVDYLGL 	PYODEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSS 	SSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV 	SQIHTDAAKENTCYCGAVAKRQEKKGMEPLOGHATPALP 	SLSASTSVSDSSQKKEEHNYSLFVSDNLGE 	EEEDYEDDKDDDI
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357 LPQLQTLLTLSQQQQSNSSSTSPYEIYHSTPQKPQQQQLSASFSPGSQASQSPLTP---- 412
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                                                                                                                    ---PPPPHANRPOYOMVKSRNM------OELIKKGFPMSSP
                                                                                                                                                                                                                                                                305 QEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDV
                                                                                                                                                                                                                                                                                        393 EDDKODDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQERML--
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Publication No. US20050106579A1
GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Requiated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/17, 665
CURRENT PILING DATE: 2003-11-21
PRIOR PILING DATE: 2002-06-10
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SOFTWARE: Patentin version 3.1
SEQ ID NO 75
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US-10-717-665-75
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Matches 8
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                                                                                                                                              RRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVSELPLTARPRSRKEKNKLAFRACRL
                                                                                                                                                                         KKKAQYBANKVKLWGLNTEYDNLLFVINSIKQBIVNRVQNPRDERGPNMGQKLBILIKDT
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EXPRESSION OF 10,000 OR MORE
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                                                       TSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKS
                                                                                                TSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKS
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| Sequence 31914, Application US/11097143
| Publication No. US2005020855841
| GENERAL INFORMATION:
| APPLICAMT: et al. |
| TITLE OF INVENTION: ETECTION KIT, SUCH AS NUCTITLE OF INVENTION: DETECTION KIT, SUCH AS NUCTITLE OF INVENTION: DETECTION KIT, SUCH AS NUCTITLE OF INVENTION: DETECTION KIT, SUCH AS NUCTITLE OF INVENTION: DATEAYS, FOR DETECTING EXPERIENCE: CLOOM728
| CURRENT FILING DATE: 2005-04-04
| PRIOR APPLICATION NUMBER: 60/157,832
| PRIOR APPLICATION NUMBER: 60/160,191
| PRIOR FILING DATE: 1999-10-19
| PRIOR PILING DATE: 1999-10-28
| PRIOR APPLICATION NUMBER: 60/161,932
| PRIOR APPLICATION NUMBER: 60/161,932
| PRIOR APPLICATION NUMBER: 60/173,383
| PRIOR APPLICATION NUMBER: 60/175,693
| PRIOR APPLICATION NUMBER: 60/175,693
| PRIOR PILING DATE: 1999-11-22
| PRIOR APPLICATION NUMBER: 60/175,693
| PRIOR PILING DATE: 2000-00-24
| PRIOR APPLICATION NUMBER: 60/191,637
| PRIOR PILING DATE: 2000-00-23
| NUMBER OF SEQ ID NOS: 43008
| SEQ ID NO 31914
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US-11-097-143-31914
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209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
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209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS 268
                                                                                                             269 SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
                                                                                                                                                                             -----DVDDED 368
                                                                                                                                                                                                     326 N-----DNKODEREQETDEEDEEDDEEDDEEDDEEDDEEDDEEDDEEDDEE 379
                                                                                                                                                                                                                                                                                                             380 DDEEDDEEDDEEDBEEDBEEDBEEDBEDDDDDDDDDSD-----EDDEEEDKKEDBEDGGDGN 433
                                                                                                                                                                                                                                                                               369 HDEGFGSEHELSENEEEEEEEDYEDDKODDISDTFSEPGYENDSVEDLKE----- 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA TITLE OF INVENTION: TO Genomic Host DNA FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/10/294,804
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/410,399
PRIOR FILING DATE: 1999-10-01
SUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 ATPALPF--KETQELLL----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH
                                                                       286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 196.5; DB 4; Length 1162; 24.2%; Pred. No. 0.00056;
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                                                                                                                                                                                  336 NYSLFVSDNLGEQPTKCSPEEDEEDEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/10294804; Publication No. US20030133948A1; GENERAL INFORMATION:
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Matches 96; Conserv
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TYPE: PRT
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; Sequence 2. Application US/09894273
; Publication No. US20040037847A1
; GENERAL INFORMATION:
   APPLICANT: Kieff, Elliott D.
   APPLICANT: Kaye, Kenneth M.
   TITLE OF INVENTION: RIADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REPERENCE: 16412-10001R
; TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REPERENCE: 16412-10001R
; FILE REPERENCE: 1900-10-6-28
; FILE REPERSON NUMBER: US 60/109,422
; RUGHE PLICATION NUMBER: US 60/109,422
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPWR 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 160;
                                             Sequence 59634, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
FILE REFERENCE: 790C1P3/US;
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US/08631
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR PLILING DATE: 2000-03-31
; PRIOR SEQ ID NOS: 60736
; SOFTWARE: CUSCOM
; SEQ ID NO 59634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 2.3e-05;
2; Mismatches 12;
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Best Local Similarity 73.0%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-10-450-763-59634
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66 DTL 68
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------PO 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYSLFVSDNLGEQPTKCSPEEDEEDEE 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.9%; Score 196.5; DB 5; Length 1162; Best Local Similarity 24.2%; Pred. No. 0.00056; Matches 96; Conservative 52; Mismatches 145; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 HDEGFGSEHELSENEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15 (5.796) C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 PPPSQQTTPPHSPTTPPPBPSKSSPDSLAPSTLRSLRKRRLSS-
                                                         434 KTLSIQSSQQQEPQQQE-PQQQEPQQQEPLQEPQQ 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 -VTSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSE 454
                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-10-194-046-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT / ORGANISM: Kaposi's sarcoma-associated herpesvirus (US-10-732-923-3319)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3319, Application US/10732923 Publication No. US20050108791A1 GENERAL INFORMATION:
Sequence 2, Application US/10194046 Publication No. US20040248081A1 GENERAL INFORMATION:
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SEQ ID NO 3319
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                                                                                                                             124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA
                                                                      Gaps
                                                                87;
Length 1003;
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APPLICANT: RICHARDSON, Thomas W.; WARREN, Bridget A.;
APPLICANT: GRIFFIN, Jennifer A.; TANG, Y. Tom;
APPLICANT: GRIFFIN, Jennifer A.; TANG, Y. Tom;
APPLICANT: EMERLING, BROOKE M.; LAL, Preeti G.;
APPLICANT: EMERLING, BROOKE M.; LAL, Preeti G.;
APPLICANT: EMERLING, Brooke M.; Lol, Preeti G.;
APPLICANT: BARKUMAR, Jayalaxm; LI, Joana X.;
APPLICANT: BARKUMAR, Madhusudan M.; LEE, Ernestine A.;
APPLICANT: SANJANWALA, Madhusudan M.; LEE, Ernestine A.;
APPLICANT: SANJANWALA, Mathusudan M.; LEE, Rooker, SANJANWALA, Mathusudan M.; Lie, Y. APPLICANT: BOROWSKY, Mark L.; YAO, Monique G.;
APPLICANT: BARROSO, Ines; TRAN, Bao;
APPLICANT: WALIA, Narinder K.; HAFALIA, April J. A.;
APPLICANT: NGUYEN, Danniel B.; LU, Yan;
TITLE OF INVENTION: NUCLEIC ACID-ASSOCIATED PROTEINS
   Query Match 5.8%; Score 194.5; DB 5; Length Best Local Similarity 24.5%; Pred. No. 0.00063; Matches 94; Conservative 55; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                          TILE REFERENCE: PF-1068 USN
CURRENT APPLICATION NUMBER: US,10/483,505
CURRENT FILING DATE: 2004-12-12
CURRENT FILING DATE: 2004-12-12
PRIOR PELING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/305,089
PRIOR FILING DATE: 2001-07-12
PRIOR PILING DATE: 2001-07-12
PRIOR PILING DATE: 2001-07-12
PRIOR PLING DATE: 2001-07-12
PRIOR PLING DATE: 2001-07-12
PRIOR PLING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/305,390
PRIOR PLING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-14
PRIOR FILING DATE: 2001-07-19
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LENGTH: 427
TYPE: PRT
ORGANISM: Candida albicans
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US-10-032-585-7386
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; ORGANISM: HOI
US-10-487-593-1
SEQ ID NO 7386
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Publication No. US20030180953A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey,
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT PILING DATE: 2001-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                    178 ISRAAAPVCSSKTLQAEVPLSDCVQK----ASKPPSSTQIMVKTNMYHNEKVNFHVECK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                            107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 -----SPTPD---GSERIGLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 G-----EQPTKCSPEEDEEDVD-----DEDHDEGFGSEHELSENEEEEEEDYED 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 DKDD------DISDTFSEPGYENDSVED----LKEVTSISSRKRGKRRYFWEYSEQLT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443 PSQQERMLRPSEWNRD-TLPSNMYQKNGLHHGKY----AVKKSRRTDVEDLTPNPKKLL 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               538 -----CRLKKKAQYEANKVKLW----GLNTEYDNLLFVINSI-KQEI----VNRVQNPRD 583
                                                                                                                                                                                                                                                                                                                                                                 69
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                                                                                                                                                                                                                                                                                                                                                                                                                              233 DYVKKAKVKINPVQOSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 IKSNNHENVSLAKAKGVWSTL-PVNE------KKLNLAFRSARSVILIFSVRESG
                                                                                                                                                                                                                                                                                                                                                                 16 LDDILTEVPEQDDELYNPESEQDKWEKKGSKRKSDRM---ESTDTKROKP---SVHSRQL
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                               120 LDDFSS--PYQDEEVISKTFTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKI
                                                                                                                                                                                                                                                Query Match
5.7%; Score 189.5; DB 5; Length 735;
Best Local Similarity 23.1%; Pred. No. 0.00089;
Matches 134; Conservative 78; Mismatches 199; Indels 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 DERDOKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERK-
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                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7037554CD1
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 735
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                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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US-10-032-585-7386
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182 NNWAALRESLARIELPWSKHSFIEHQSITSADKTESEIK--DIYDDTERELAFYKQGLD- 238
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                                                                                                                                                                                               371
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                                                                                                                                                                                                                                                                                    426 RKRG------KRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHH 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                    239 ---AVKQSRKT------LLKLKIPFSRPMDYFAEMVKSDE------HMDKLKNK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAFRACRLKKKAQYEANK---VKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 GFGSEHELSENEEEEE-----EEEDYEDDKDDISDTFSEPGYENDSVEDLKEVTSISS
                                                                197 LSDCVQKA-SKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV--KINPVQQSRPLLS
                                                                                                                                                                                                 314 GESSSLSASTSVSDSSOKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDE---DHDE
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                                 69; Mismatches 150; Indels 152;
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DB 4; Length 427;
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Best Local Similarity 19.5%; Pred. No. 0.044;
Matches 165; Conservative 87; Mismatches 288
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                 Pred. No. 0.0021
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                                                                                                                                                       61 --KSNTKKDDDDYQSEVLSKKEQRRLKKLQ-
 Query Match
Best Local Similarity 22.2%
Matches 106; Conservative
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549 NKVKL
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LENGTH: 707
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US-10-384-569-3
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Best Local
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APPLICANT: Hovanessian, Ara
APPLICANT: Hovanessian, Christian
APPLICANT: Jacotot, Etienne
APPLICANT: Muller, Sylviane
APPLICANT: Muller, Sylviane
APPLICANT: Guichard, Gales
TITLE OF INVENTION: A NOVEL CELL SURFACE RECEPTOR FOR HIV RETROVIRUSES,
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USES.
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                                                            SDPDFMYELDRE-MNYQQNPRDNF---LSLEDCKDIENLESFTDVLDNEG
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APPLICANT: HOVANESSIAN, ARA G.
APPLICANT: HOVANESSIAN, ARA G.
APPLICANT: HOVANESSIAN, JEAN-PAUL
TITLE OF INVENTION: INHIBITION OF VIRUS ANCHORAGE BY RGG DOMAIN OF A CELL SURFACE-
TITLE OF INVENTION: THERAPEUTIC USES THEREOF BY INHIBITION OF MICROORGANISM OR
TITLE OF INVENTION: PROTEIN LIGAND BINDING TO THE CELL-SURFACE-EXPRESSED PROTEIN
FILE REFERENCE: 03495.026.0000
CURRENT APPLICATION NUMBER: US/10/384,569
CURRENT APPLICATION NUMBER: 2004-07-14
PRIOR APPLICATION NUMBER: 60/363,371
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20.4%; Pred. No. 0.0088;
vative 76; Mismatches 162; Indels 148; Gaps
                   CURRENT APPLICATION NUMBER: US/09/825,886
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 09/393,302
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: PCT/EP98/01409
PRIOR APPLICATION NUMBER: PCT/EP98/01409
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver: 2.1
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Publication No. US20040002457A1
GENERAL INFORMATION:
FILE REFERENCE: 03495.0166-01000
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US-09-825-886-22
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ORGANISM: Homo sapiens
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Squence 19, Application US/10400083

Publication No. US20040186056A1

GENERAL INFORMATION:
APPLICANT: Rucelahti, Erki

APPLICANT: Christian, Sven
TITLE OF INVENTION: HMAN 2 Peptides and Related Molecules
TITLE OF INVENTION: HMAN 2 Peptides and Related Molecules
TITLE OF INVENTION: HMAN 2 Peptides and Related Molecules
TITLE OF INVENTION: HMAN 2 Peptides
TITLE OF INVENTION: HAT Selectively Home to Tumor Blood Vessels and Tumor Cells
TITLE OF INVENTION NUMBER: US 10/116,866

PRIOR FILING DATE: 2002-04-05

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 19

LENGTH: 707

TAVER. DATE: 2002

LENGTH: 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGP 308
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    PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION WUMBER: 60/397,600
PRIOR FILING DATE: 2002-07-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PALENTIN VEr. 2.1
SEQ ID NO 3
LENGTH: 707
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                                                                                                                                       TYPE: PRT;
ORGANISM: Homo sapiens
US-10-384-569-3
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APPLICANT: Liao, X. Charlene
APPLICANT: Liao, X. Charlene
APPLICANT: Liao, X. Charlene
APPLICANT: Masuda, Esteban
APPLICANT: Radel Pharmaceuticals, Inc.
APPLICANT: Rigel Pharmaceuticals, Inc.
FILE REFERENCE: 021044-000330US
CURRENT PLILNG DATE: 2004-04-011
PRIOR PRICATION NUMBER: US 60/327,212
PRIOR FILING DATE: 2001-10-03
PRIOR FILING DATE: 2001-10-03
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 96
SECTION OF THE PARTICAL OF TH
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ch 5.2%; Score 174; DB 4; Length 707; 1 Similarity 20.4%; Pred. No. 0.0088; 99; Conservative 76; Mismatches 162; Indels 148;
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Best Local Similarity 20.4%; Pred. No. 0.0088;
Matches 99; Conservative 76; Mismatches 162; Indels 148; Gaps
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                                                                                                      February 28, 2006, 08:56:26; Search time 17.0827 Seconds (without alignments) 556.876 Million cell updates/sec
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1 MPQPSVSGMDPPFGDAFRSH......TAEGNPTGGLVGLRIPTSKV 639
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*

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7: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USII NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-124-367A-292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-770-726-49
                                                                                                                                                                                                                                                                                                    117670 segs, 14887254 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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905, App 2, Appli 2964, Ap 1120, Ap	14, Appl 415, App 28, Appl 29, Appl	2050, Ap 2755, Ap 950, App 968, App	0 - 4 D	962, App 958, App 960, App
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US-10-821-234-905 US-11-128-572-2 US-10-793-626-2964 US-10-821-234-1120	US-11-024-959-415 US-11-024-959-415 US-11-135-855-28 US-11-135-855-29	US-11-072-512-2050 US-11-072-512-2755 US-10-453-372-950 US-10-453-372-968	US-110-453-72-775 US-11-098-686-10232 US-110-821-234-1039 US-11-241-056-14 US-10-528-031-8	US-10-453-372-962 US-10-453-372-958 US-10-453-372-960
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25 24 28 28	3010	9 W W W W V	2 6 4 4 4 2 6 0 1 2	4 4 4 5 4 4

ALIGNMENTS

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276 KKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVESTIGATION: NOVEL FULL LENGTH CDNA FILE REPERENCE: 084335-0191 CURRENT APPLICATION NOVEL FULL LENGTH CDNA CURRENT APPLICATION NUMBER: US/11/072,512 CURRENT FILING DATE: 2005-03-07 PRIOR APPLICATION NUMBER: US 60/350,978 PRIOR FILING DATE: 2002-01-25 PRIOR APPLICATION NUMBER: JP 2001-379298 PRIOR FILING DATE: 2001-11-05 NUMBER OF SEQ ID NOS: 4096 SOFTWARE: Patentin Ver. 2.1
        Sequence 2651, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                          APPLICANT: ISOGAL, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
                                                                                                                                                                                                                                                                                           NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
VOSHIKAWA, ISUTOMU
OTSUKA, MOTOYUKI
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Best Local Similarity 21.9<sup>3</sup>
Matches 74; Conservative
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US-11-072-512-2651
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US-11-072-512-2651
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Sequence 2, Application US/10509422; Publication No. US20050244825A1; GENERAL INFORMATION:
                                                                                                                               Sequence 1, Application US/11128660
Publication No. US20060024324A1
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                                                                 RESULT 3
US-11-128-660-1
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APPLICANT: INSTITUT PASTEUR
APPLICANT: DRUILHE, PIERRE
TITLE OF INVENTION: IDENTIFICATION OF A CONSERVED REGION OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: MSP3 TARGETED BY BIOLOGICALLY ACTIVE ANTIBODIES
FILE REFERENCE: 275601US0
CURRENT APPLICATION NUMBER: US/11/189,817
CURRENT PILING DATE: 2005-07-27
PRIOR FILING DATE: 2006-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                           357
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                                                                                                                                                                                                                                          467
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                                                                                                                                         196 KKAAKVVPVKAKNVAEDEDEBEEDDEDEDDDEDDEDDEBEEEEEEEEFVKEAPG
                                                                                                       --LSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKEVTSISS
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l Similarity 20.9%; Pred. No. 0.0016;
82; Conservative 61; Mismatches 146; Indels 104; Gaps
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Publication No. US20060030006A1
GENERAL INFORMATION:
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US-11-189-817-2
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
LENGTH: 354
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APPLICANT: Statens Serum Institut
TITLE OF INVENTION: Vaccines comprising chimeric malaria proteins derived from Plasmoc
TITLE OF INVENTION: falciparum
FILE REFERENCE: 15007dk
CURRENT APPLICATION NUMBER: US/11/128,660
CURRENT FILING DATE: 2005-05-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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4.7%; Score 157.5; DB 7; Length 651;
Best Local Similarity 18.4%; Pred. No. 0.0076;
Matches 99; Conservative 99; Mismatches 171; Indels 169
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TITLE OF INVENTION: Human BMP2 Inducible Kinases
FILE REFERENCE: 004974.01015
CURRENT APPLICATION NUMBER: US/10/509,422
CURRENT FILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: PCT/EP03/080825
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2005-05-09

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CURRENT FILING DATE:
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APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CLO01519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
                                                                                                                                                                                                                                       Query Match
4.6%; Score 155; DB 6; Length 1168;
Best Local Similarity 18.8%; Pred. No. 0.023;
Matches 117; Conservative 81; Mismatches 189; Indels 236;
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PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION UNMERR: US 60/367,512
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 2
IENGTH: 1168
TYPE: PRI
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371 RLDEVISKYAMLQDKSEEGGERKKRRARLQGTSSHS---ADTPEASLD--SGEGPSGMASQ 425
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Genetic Polymorphisms of Detection and Uses Thereof
FILE REFERENCE: CLOOISIS.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-06-25
PRIOR PILING DATE: 3004-06-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                4.6%; Score 154; DB 7; Length 740;
22.0%; Pred. No. 0.015;
tive 63; Mismatches 162; Indels 130;
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PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/592,609
PRIOR PILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 293
LENGTH: 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 292, Application US/11124367A; Publication No. US20060024700A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 22.03
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-124-367A-293
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US-11-124-367A-292
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Liu, wei
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REPRERNCE: AM10.1079; (0.31896-0.10000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-0.2-04
NUMBER OF SEQ ID NOS: 48640
SOFWMARE: Patentin version 3.2
                                                 24;
                                                                                                                        181 AAAPVCSS----KTLQAEVPLSDCVOKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKKKKAQ-----YEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKL 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 DIWGTKEVDYLGLDDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSWKVKTLDEI-LOEKKRRKEOEE---KABIKRLKNSDDRDSKRDSL-----EEGE 52
                                                                                          124 SSPYQDEEV---ISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKONPLPSSFPGKKITSR
                                                                                                                                                                                                                                                                                                                      ------KOAPEPLRAEARVAIPASVLP
                                                                                                                                                                                                                                                                                                                                                                      294 -----ETQELLLSPLPQEGPGSLA---AGESSSLSASTSVSDSSQ-----KKEEHN
                                                                                                                                                                                                                                                                                                                                                                                                561 NOSHETLERENQECPRSLEEDLETLKSLEKENKRAIKGCGGSETSRKRGCR-----Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 KAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 YSLFVSDNLGEQPTKCSPEEDEEDVD-DEDHDEGFGSEHEL--SENEEEEEEEDYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---SISSRKRGKRRYFWEYSEQ
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                                                    Gaps
                                                 Indels 173;
    DB 6, Length 1618,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 795;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      773 OMTLRPPEKVDLEPLKSLDQEIARPLENENQËFLKSLKËESVË 815
4.4%; Score 147.5; DB 6;
19.9%; Pred. No. 0.1;
tive 90; Mismatches 204;
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20.2%; Pred. No. 0.056;
tive 80; Mismatches 214;
                                                                                                                                                                                                                                 379 ARTPILASTPIPPTPOAPSPAVDAEIRAQDAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 DDKDDDISDTFSE-PGYENDSVEDLKEVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49, Application US/10770726
Publication No. US20050266409A1
    Query Match
Best Local Similarity 19.9%
Matches 116; Conservative
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APPLICANT: Alewski, Hendrik
APPLICANT: Zulewski, Hendrik
APPLICANT: Vallejo, Mario
TITLE OF INVENTION: METHOD OF TRANSPLANTING IN A MAMMAL AND TREATING DIABETES MELLITU
TITLE OF INVENTION: A NESTIN-POSITIVE PANCREATIC STEM CELL
TITLE OF INVENTION: A NESTIN-POSITIVE PANCREATIC STEM CELL
TITLE OF INVENTION: A NESTIN-POSITIVE PANCREATIC STEM CELL
TITLE OF INVENTION: A NUBER: US 09/731,255
PRIOR FILING DATE: 2000-11-06
PRIOR FILING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 60/15,109
PRIOR APPLICATION NUMBER: US 60/215,109
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                157
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                                                                                                                                                                                                                                                                                                                                       : :: | | :| | :| | :| | 286 EVNRRIERLINKPGPDTFPDYGDVLRAVEKAAARHSLGLPRQQLQLMAQDAFRDVG---- 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TCYCGAVAKRQE---KKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAA- 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 GESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGF 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 488 EQMQEGQEDDEEEDEEERAAAGKDGDKSPMSSLQISNEKNLEPGKQISRSSGEQQNKGRI 547
                                                                                                                                                                                                                                                           228 KELDLSELDDPDSAYLQEARLKRKLIRLFGRLCEL--KDCSSLTGRVIEQRIPYRGTRYP
                                                                                                                                                                                                                                                                                                                                                                                                                            113 KEVDYLGLDDFSSPYQDE----EVISKTPTLAQLNSEDSQSVSDSLY-----YP
                                                                                                                                                                                                                                                                                                        DSLFSVKO---NPLPSSFPGKKITSRAAAPVCSSKTL----OAEVPLSDCVQKASKPPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 FWEYSEQLTPS-QQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNP
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                                                                                                                                                                     Gaps
                                                                                                                      4.6%; Score 154; DB 7; Length 760;
22.0%; Pred. No. 0.015;
Live 63; Mismatches 162; Indels 130;
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                                                                                                                        Query Match
Best Local Similarity 22.09
Matches 100, Conservative
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CORGANISM: Homo sapiens
US-10-984-645-2
         ; LENGTH: 760
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426 AAECAQEAE------PPKSEESFRSREAEEGQEGQDAMSRAKANWIRAFNKVRMQLQ 476
                                                                                                                                                                                                                                                            LP------VPSSQCCNWNYFGWGEQNDDPDSA-VDDRDSDY 200
                                                                                                                                                                                                                                                                                                                                                     247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q----EDITVAEPKEPKRISFPTAAPQK----EDKVSAVPIEAPDVSKGIPKAATPEEKA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                        ------FSEPR--ALSP----TGSSRYASSGELSQGSSQLSEDFDPDEH 284
                                                                                  64 -VWNKGLI------WDTMVGTVWIPLRTIRQSNEEGPGEWLTLDSQAIMADSEICGTKDP 116
                                                                                                                                DY--LGLD-DFSSPYQ--DEEVISKTPTLAQLNS---EDSQSVSDSLYYPDSLFSVKQNP 167
                                                                                                                                                                                                                       LPSSFPGKKITSRAAAPVCSSKTLQAEVPLSDCVQ-----KASKPPSSTQIMVKTNMY 220
63
                                                                                                                                                                                                                                                                                                                                              201 RSETSNSIPPPYYTTSQPNASVHQYSVRP----PPLGSR-----ESYSDSMHSYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 KAQYEANKVK-LWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTL
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                                                                                                                                                                           117 TFHRILLDAHFELPLDIPEEBARYWAKKLEQLNAMRDQDEYSFQDQ------QDKP
                                                                                                                                                                                                                                                                                                            221 HNEKVN-----FHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQE
                                                                                                                                                                                                                                                                                                                                                                                                 276 KKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH
                                           ----EDLTKYTK--LTSCDIWGTKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 NYSLFVSDNLGEQPT-----KCSP--EEDEEDEEDVDDEDHDEGFGSEHELSE-
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4.3%; Score 144; DB 6; Length 1404;
Best Local Similarity 19.8%; Pred. No. 0.14;
Matches 141; Conservative 132; Mismatches 268; Indels 172;
    ---LDLGLTVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 GLPV----AGQTS-----EFVNQVLEKTAE 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  520 AMSLVQSRKAĞITSALASSTLNNEELKNHVYKKTLQ 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DATABASE ACCESSION NUMBER: humangp/chr12-q14221
; DATABASE ENTRY DATE: 2003-04-22
US-10-878-556A-169
  25 TLKVQNVKSTTIAVRGSQPSWEQDFMFEINR--
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                                                77 VLDNEGALTSNWEOWDTYC---
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LENGTH: 1404
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APPLICANT: ASHERY, Uri
TITLE OF INVENTION: UNC.13 IN THE MODULATION OF NEUROTRANSMISSION AND SECRETION EVENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37;
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166 DRLEQLERKRERERKWREQQKEQKERERRABERRKEREARREVSAHHRTWREDYSDK 225
                                                                                                                                                                                                                                                                                                                                   226 VKASHWSRSPPRPPRERFEL-----GDGR-KPGEARPARAQKPAQLKBEKMEERD-- 274
                                                                                                                                                                                                                                                                                                                                                                                   339 LFVSD--NLGEQPTKCSPEED-----EEDEEDVDDEDHDEGFGSEHELSENEEEEEE 388
                                                                                                                                                                                                                                                                                                                                                                                                                            275 -ILSDLODISDSERKTSSAESSSAESGSGSEEEEEEEEEEEGSTSE----ESEEEEEE
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CURRENT APPLICATION NUMBER: US/10/495,083
CURRENT FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: PCT/EP02/12072
PRIOR APPLICATION NUMBER: EP 01 12 6235.9
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 12
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Publication No. US20060008800A1
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APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFIC
TITLE OF INVENTION: PROTEIN INTERACTIONS IN VERTEBRATE CELLS
FILE REFERRNCE: HWW-056.25
CURRENT APPLICATION NUMBER: US/10/475,204
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/US02/13008
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
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Publication No. US20050277116A1
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SEQ ID NO 34
LENGTH: 943
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CORGANISM: Homo sapiens
US-10-475-204-34
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----PDSLFSVKQNPLPSSFPGKKI 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : ||:: |: |: ||: || 335 AESTALFQGRKSREKHHNILPKTLANDKHSHKP---HPVETSQPSDKTVLDTSYALIDET
                                                                                                                                                                                         -----AKKRETYTFENSVNML-------PSSTEVSVKT----KKRLNFDDKVMLKKIE
                                                                                                                                                                                                                                                                                         220 IDNKVSDBEDKTSEGGERKPSGSSQNRIRDSEYEIQRQAKKSPSTLFLFTFVKRKSES---
                                                                                                                                                                                                                                                                                                                                                               280 EPLOGHATPALP------FKETQELLLS----PLPQEGPGSLAAGESSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 SASTSVSDSSQKKEEHNYSL---FVSDNLGEQPTKCSPREDEE--DEEDVD-----DED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : ::|; |:| |: | 332 VNNYRSTKYEMYEREQEDVGQSKDENIHTSHITQ
                                                                                                                                                                                                                                                            231 CKDYVKKAKVKINPVQQSRPLLS------QIHTDAAKE-NTCYCGAVAKRQEKKGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SDIFSEPGYE--NDSVEDLKEVTSISSRKRG-----KRRYFWEYSEQLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 DEFQRNSDRNMEEHEEMGNDCVSK-KQMPPVGSKKSSTRKDKEESKKKRFSSESKNKLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511 BEVTSTVTKSRRISRRPSDWWVVKSEESPVYSNSSVRNELPMHH-----NSSRK-----
                                                                                                                                                        178 TSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNF------HVE
71; Mismatches 147; Indels 168; Gaps
                                                                                   APPLICANT: Messes et al.

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-240CIP
CURRENT APPLICATION UNDBER: US/11/054,281
CURRENT PILING DATE: 2005-02-08
FRIOR PELING DATE: 2001-01-11
PRIOR PAPLICATION NUMBER: 60/261,014
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,013
PRIOR PILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/261,026
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,026
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/313,170
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/313,170
PRIOR APPLICATION NUMBER: 10/044,564
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 00/201-11
                                                  131 EVISK-TP---TLAQLNSEDSQSVSDSLYY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 107, Application US/11054281
Publication No. US20060013813A1
GENERAL INFORMATION:
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560 --STKKTNQSSKNIRK 573
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     Matches 110; Conservative
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SEQ ID NO 107
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US-11-054-281-107
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Sequence 305, Application US/11124368A

Sequence 305, Application Wo. US20050287559A1

GENERAL INFORMATION:

APPLICANT: Michele Cargill

APPLICANT: May Luke

TITLE OF INVENTION: Generic Polymorphisms Associated with

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof;

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof;

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof;

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof;

FILE REFERENCE: CL001524

CURRENT APPLICATION NUMBER: US 60/568,845

PRIOR FILING DATE: 2004-05-07

PRIOR PILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-11-09

NUMBER OF SEQ ID NOS: 21112

SOFTHARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 DLTKYTKLT-----SCDIWGTKEVDYLGLDDFSSPYQD-EEVISKTPTL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | : : | 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----IGNELRKIN----KVISDLTPVSELPLTARPRS----RKEKNK 532
                                                                                                                                                                                                                                                                                                                               ------GFVEKLQKKADIG--LPYPQRVVQ 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAFRACRLKKKAQYEANKVKLW-----GLNTEYDNLLFVINSIKQEIVNRVQNPRDERG
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                                                                                                                                                                               NYS-----LFVSDNLGEOPTKCSPEEDEEDBEDV--DDEDH-DEGFG---SEHELSENE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 LEDCKDIENL------ESFTDVLDNEGALTS-NWEQWDT------YCE
                                                                            G--HATPALPFKETQELLLSPLPQEGPGSL-----AAGESSSLSASTSVSDSSQKKEEH
                                                                                                                350 ĠBPBPSPVLDCVSAQMSLSE-PQEHRYTLRTSPRRAAPTRGSPTKNSSPYRENGQFBEN
                                                                                                                                                                                                                      409 NLSPNETNATVSDNVSQSPT--NPGEISQNEKGICCDSQNNGSEGVSKPPSEARLNIGHL
                                                                                                                                                                                                                                                                                             384 -EEEEEEEDYEDDKDDDISDTFSEPGYENDSV----EDLKEVTSISSRKRGKRRYFWEY
                                                                                                                                                                                                                                                                                                                                                                                                        438 SEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.2%; Score 140.5; DB 7; Length 2801; 19.9%; Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587 PNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEK-TAEGNPTGG 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              524 LESLGRHOREALKNPI-----
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Best Local Similarity 19.9%
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-11-124-368A-305
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Sequence 142, Application No. US20050250180A1

GENERAL INFORMATION:

APPLICANT: Jacobb, Kenneth

APPLICANT: Javobb, Kenneth

APPLICANT: Barie, Edward R

APPLICANT: Racie, Lisa A

APPLICANT: Brans, Cheryl

APPLICANT: Spaulding, Vikki

APPLICANT: Spaulding, Vikki

TITLE OF INVENTION SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

TITLE OF INVENTION SECRETED PROTEINS AND FOLYNUCLEOTIDES ENCODING THEM

FILE REFERENCE: 00766.000091.10

CURRENT APPLICATION NUMBER: US/10/689,742

CURRENT APPLICATION NUMBER: US/10/46,783

PRIOR APPLICATION NUMBER: 2000-1.2-21

NUMBER OF SEQ ID NOS: 231

SOFTWARE: PATENTING DATE: 2000-1.2-21

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 QOSRPLLSQIHT------DAAKENTCYCGAVAKRQEKK------GME--PLQ 283
                                                                                                                                                                                                                      293 KETOELLLSPLP-----QEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSD 343
                                                                                                                                                                                                                                                                            99 ----EIIKSPSDPKQYRYIKLQNGLQALLISDLSNVEGKTGNATDEEBEBEB-----BE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                             403 TFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNR--DTL 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 NSSDPDFMYELDREMNYQQ-----NPRD-----NFLSLEDC--KDIENLESFTDVLD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 CVQKASKPPSSTQIMVKTNMYHNEK-----VNFHVECKDYVKKAKVKIN-----PV
                                                                                                                                                     250 PLLSQIHTDAAKENTCYC-----GAVAK----ROEKKGMEPLOGHATPALPF
                                                                                                                                                                                                                                                                                                                                 344 NLGEQPTKCSPEEDEEDVDDEDHDEGFGSEHELSENEEEE-REERDYEDDKDDDISD
                                                              74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 903;
  Query Match
4.2%; Score 142; DB 7; Length 1229;
Best Local Similarity 24.7%; Pred. No. 0.16;
Matches 67; Conservative 47; Mismatches 83; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.2%; Score 140.5; DB 6; Length Best Local Similarity 20.2%; Pred. No. 0.14; Matches 142; Conservative 109; Mismatches 227; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PSNMYQKNGLHHGKYAVKKSRRTDVEDL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 LVETRNLYGVVG-----AESRSAPVEHL 273
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ORGANISM: Homo sapiens
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US-10-689-742-142
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                                                                                                                                                                                                 2240 -----SLTAGKATKIPCESPPLEVVDTTASTKRHLRTRVQKVQVKEEPSAVKFTQTSG 2292
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2396 VKÉELLAVGKLIQTSGETTHTDKEPVGBĠKGTKAFKQPAKRKLDAEDVIGSRRQPRAPKE 2455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
                                  2089 ROLTTRKEKARALEDLVDFKE-LFSAPGHTEESMTIDKNTKIPCKSPPPELTDTAT---- 2143
                                                                                                          2293 ETTDADKEPAGE---DKGIKALKESAKQTPAPAASVTGSRRRPRAPRESAQAIEDLAGFK 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SCDIWGTKEVDYLGLDDFSSPYQD-EEVISKTFTL 139
                                                                                                                                                                                                                                                                                                                                      ----GSEHELSENEEEEEEDYEDDK 396
                                                                                  SSKTLOAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQ 246
                                                                                                                                                                   247 QS----RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSP 302
                                                                                                                                                                                                                                                      303 LPQEGPGSLAAGESSSL---SASTSVSDSSQKKEEHNYSLFVSDNLGEQP----TKCSP 354
                                                                                                                                                                                                                                                                                                                                                                                                                         397 DDDISDIFSEPGYENDSVEDLK-----EVTSISSRKRGKRRYFWEYSEQLTPS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 QOERMIRPSEWNRDTLPSNMYQKNGLHHGK----YAVKKSRRTDVEDLTPN-----PKK 494
140 AQLNS--EDSQSVSDSLYYPDSLFSV------KQNPLPSSFPGKKITSRAAAPVC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          495 LLQIGNELRKLNKVISDLTPVSEL-----PLTARPRSRKEKN---KLAFRACRLKK 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USENTIAL APPLICATION US/11124367A

Publication No. US20060024700A1

GENERAL INFORMATION:

APPLICANT: Michaele Cargill

APPLICANT: Michaele Cargill

APPLICANT: Hongjin Huang

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: BOBER: US/11/124,367A

CURRENT APPLICATION NUMBER: US/11/124,367A

CURRENT FILING DATE: 2004-05-09

PRIOR APPLICATION NUMBER: US 60/589,609

PRIOR PILING DATE: 2004-06-25

PRIOR FILING DATE: 2004-06-25

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PRIOR FILING DATE: 2004-06-36

SOFTWARE FABLICATION NUMBER: US 60/599,554

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PRIOR FILING DATE: 2004-06-36

SOFTWARE FABLICATION NUMBER: US 60/599,554

PRIOR FILING DATE: 2004-06-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 LEDCKDIENL-----ESFTDVLDNEGALTS-NWEOWDT-------YCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7; Length 2801;
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19.9%; Pred. No. 0.56;
tive 89; Mismatches 242;
                                                                                                                                                                                                                                                                                                                                        355 EEDEEDEEDVDDEDHDEGF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 19.9
Matches 131; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                           2144 STKRCPKTRPRKEVKEELSAVERLTOTSGOSTHTHKEPASGDEGIKVLKORAKKKPNPVE 2203
                                                        140 AQLNS--EDSQSVSDSLYYPDSLFSV------KONPLPSSFPGKKITSRAAAPVC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397 DDDISDIFSEPGYENDSVEDLK------EVTSISSRKRGKRRYFWEYSEQLTPS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 QOERMIRPSEWNRDTLPSNMYQKNGLHHGK----YAVKKSRRTDVEDLTPN-----PKK 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2456 KAQPLEDLASFQELSQTPGHTEELANGAADSFTSAPKQTPDSGKPLKISRRVLRAPK 2512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             495 LLQIGNELRKLNKVISDLTPVSEL-----PLTARPRSRKEKN---KLAFRACRLKK 542
                                                                                                                                                                                                                                                                                                                                                                                                                          303 LPQEGPGSLAAGESSSL---SASTSVSDSSQKKEEHNYSLFVSDNLGEQP----TKCSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------GSEHELSENEEEEEEEDYEDDK
                                                                                                                                                                                  SSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQ
                                                                                                                                                                                                                                                                                                      247 QS----RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSP
                                                                                                                                                                                                                                                                                                                                                           2204 EEPSRRRPR------APKEKAQPLEDLAGFTELSETSGHTOE----
                                                                                                    EEDEEDEEDVDDEDHDEGF-----
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                      Copyright
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- protein search, using sw model OM protein February 28, 2006, 08:45:35; Search time 38.9699 Seconds Run on:

(without alignments) 1577.691 Million cell updates/sec

US-10-717-665A-44 3349

1 MPQPSVSGMDPPFGDAFRSH......TAEGNPTGGLVGLRIPTSKV 639 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: 283416

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query	Length	DB	ID	Description
-	000		101	-	DAMA	earon - milooloum
4 (0 0		· t	4 (1011	1
7	707	9	777	7	OHOT A	4
c	188	5.6	2761	0	T29285	hetical
4	184	5.5	1089	7	S48244	eir
'n	180.5	5.4	694	7	DNCHNL	nucleolin - chicke
9	179	5.3	990	~	T38274	probable transcrip
7	174	5.2	707	~	A35804	nucleolin - human
80	168.5	5.0	1187	~	T46637	transcription fact
O	166.5	5.0	412	~	A55320	immunophilin FKBP4
10	165.5	4.9	1063	N	A40253	acidic nuclear pro
11	165	4.9	678	~	A54514	glutamic acid-rich
12	165	4.9	1038	~	S52522	hypothetical prote
13	164.5	4.9	1082	~	T50650	
14	164	4.9	916	~	522864	DNA topoisomerase
15	163.5	4.9	802	Н	S48529	NAB3 protein - yea
16	162.5	4.9	713	~	A27441	nucleolin - Chines
17	162.5	4.9	836	~	S49940	cell division cont
18	161	4.8	831	~	S39835	hypothetical prote
19	161	4.8	885	7	G71608	ATP-dept. acyl-CoA
20	160.5	4.8	1877	~	T21861	hypothetical prote
21	160.5	4.8	1974	7	T16703	hypothetical prote
22	160	4.8	500	7	S55785	nucleolar protein
23	160	4.8	1188	7	T46608	zinc finger protei
24	159.5	4.8	1128	7	G86266	hypothetical prote
25	159	4.7	736	~	G01522	
26	159	4.7	1085	7	S55352	IFH1 protein - yea
27	159	4.7	1115	7	T41342	probable coiled-co
28	158.5	4.7	1611	7	T38236	hypothetical prote
53		4.7	3488	7	T34418	

A;Cross-references: UNIPARC:UP1000016CF68; GB:M22089; NID:g200111; PIDN:AAA19841.1; PID:c C;Comment: This housekeeping protein is involved in the synthesis, packaging, and maturat

A;Residues: 1-44 <RES>

A; Introns: 6/3, 45/3; 211/1; 273/1; 302/1; 349/2; 391/1; 432/3; 484/1; 525/2; 566/1; 608, C; Superfamily: nucleolin; ribonucleoprotein repeat homology C; Reywords: DNA binding; duplication; nucleus; phosphoprotein; RNA binding; transcriptior F;310-375/Domain: ribonucleoprotein repeat homology <RRM1> F;311-316/Region: RNA-binding RNP2 motif F;311-316/Region: RNA-binding RNP2 motif F;349-356/Region: RNA-binding RNP1 motif

F;396-458/Domain: ribonucleoprotein repeat homology «RRM2» F;397-402/Region: RNA-binding RNP2 motif F;431-438/Region: RNA-binding RNP1 motif F;488-551/Domain: ribonucleoprotein repeat homology «RRM3» F;489-494/Region: RNA-binding RNP2 motif

hypothetical prote	hypothetical prote	SIS2 protein - yea	myosin-like protei	Alzheimer's diseas	major merozoite su	hypothetical prote	hypothetical prote	Fas-binding protei	erythrocyte-bindin	myelin transcripti	oxysterol-binding	nestin - golden ha	hypothetical prote	hypothetical prote	hypothetical prote
T38495	T24541	S38149	S38173	A49795	A45948	T00365	T01029	T03847	A37793	T30189	847536	T34518	T38817	867701	T42963
7	7	7	~	ч	~	~	~	~	~	N	~	~	N	7	~
1969	1151	262	1875	695	1726	1280	669	740	1435	1182	1190	1804	992	610	792
4.7	4.7	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6
158	157.5	157	156.5	156	156	155.5	155	155	155	154.5	154.5	154	153.5	153	153
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C.Date: 30-Sep-1992 #Bequence revision 30-Sep-1992 #text_change 09-Jul-2004
C.JACCEBSION: A29958; A40769; Ā56240; 184688
R.BOUTDON, H.M.; Lapeyre, B.; Amalric, F.
J. Mol. Biol. 200, 627-638, 1988
A;Title: Structure of the mouse nucleolin gene. The complete sequence reveals that each F.
A;Reference number: A29958; MUID:88316930; PMID:3137346
A;Accession: A29958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT: P09405; UNIPARC: UPI0000009C3; GB:X07699; NID:g53453; PIDN:C7 R;Pasternack, M.S.; Bleier, K.J.; McInerney, T.N. J. Balol. Chem. 266, 14703-14708, 1991 J. Ashilo: Chem. 266, 14703-14708, 1991 Ashilo: Granzyme A binding to target cell proteins. Granzyme A binding to target cell proteins. Granzyme A binding to Larget cell proteins. Granzyme A binding to Larget Dinchelms. A;Reference number: A40769; MUID:91317840; PMID:1860869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ryang, T.H.; Tsai, W.H.; Lee, Y.M.; Lei, H.Y.; Lai, M.Y.; Chen, D.S.; Yeh, N.H.; Lee, S. Mol. Cell. Biol. 14, 6068-6074, 1994
A;Title: Purification and characterization of nucleolin and its identification as a trans A;Reference number: A56240; MUID:94344117; PMID:8065340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Bourbon, H.
Gene 68, 73-84, 1988
A;Title: Sequence and structure of the nucleolin promoter in rodents: Characterization of
A;Reference number: 148118; MUID:89121496; PMID:2906027
A;Reference number: 148118; MUID:89121496; PMID:2006027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: protein
A,Residues: 2-19,558-567 <YAN>
A,Cross-references: UNIPARC:UP100001739D0; UNIPARC:UP100001739D1
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 2-20,'X',22-24 <PAS>
A;Cross-references: UNIPARC:UP100001739CF
                                                                                                                                 Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-707 <BOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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                                                                                   nucleolin - mouse
RESULT 1
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A;Molecule type: protein
A;Residues: 651-703 <LIS:
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Best Local Similarity
Matches 107; Conserv
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 A; Accession: A24088
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                                                                                                                                                                                                                                                                            A; Start codon: GTG
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cipate: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 23-Jul-1999
CiAccession: JHO48; A24088; I63130
RiBourbon, H.M.; Amalric, F.
RiBourbon, H.M.; Amalric, F.
A; Hitle: Nucleolin gene organization in rodents: highly conserved sequences within three A; Reference number: JHO148; MUID:90269607; PMID:2347493
A; Accession: JHO148
A; Molecule type: DNA
A; Residues: 1-712 < BOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Title: Clustering of glycine and Ng.Ng-dimethylarginine in nucleolar protein C23.
A.Reference number: A24088; MUID:86104094; PMID:4084504
                                                                                                                              28;
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                                                                                                                                                                 196
                                                                                                                                                                                                                                         197 LSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIH 256
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                                                                                                                                                                                                                                                                            ---KAVATPAKKNITPAK----- 102
                                                                                                                                                                                                                                                                                                                                                    -----VIPTPGKKG-----VAQAKALVPTPGKKGAATPAKGA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----BEEEDYEDDK 396
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                                                                                                                                                                                                   PKEVEEDSEDEEMSEDE----DDSSGEEEVVIPOK-KGKKATTTPAKKVVVSOTKKAAVP
                                                                                                                                                                                                                                                                                                                TDAAKENTCYCGAVAKROEKKGMEPLQGHATPALPFKETQELLLSPLP-QEGPGSLAAGE
                                                                                                                                                                                                                                                                                                                                                                                      SSSLSASTSVSDSSQKKEEHNYSLFVSDN-----LGEQPTKCSP----EEDEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEOL-TPSOOERMLRPSEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402 LSFNITEDELKEVFEDAMEIRLVSQDGKSKGIAYI--EFKSB-ADAEKNLEEKQGAEIDG
                                                                                        Query Match 6.2%; Score 209; DB 1; Length 707;
Best Local Similarity 21.0%; Pred. No. 0.0012;
Matches 128; Conservative 78; Mismatches 180; Indels 224; Gaps
                                                                                                                                                                 137 PILAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSSKTLQAEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRDTLPSNMYQKN-----GLHHGKYAVKK------SRR-----TDVEDL
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A;Note: the authors translated the initiation codon GTG for :R:Lischwe, M.A.; Cook, R.G.; Ahn, Y.S.; Yeoman, L.C.; Busch, Biochemistry 24, 6025-6028, 1985
F;524-531/Region: RNA-binding RNP1 motif
F;570-634/Domain: Tibonucleoprotein repeat homology <RRM4>
F;571-576/Region: RNA-binding RNP2 motif
F;607-614/Region: RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEDVDDEDHDEGFGSEHELSENEEE---
                                                                                                                                                                                                                                                                           TP--AKKAAVTPGK------
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A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: NNA
A;Residues: 'WV', 2-44 <RES>
A;Cross.references: 'MV', 2-44 <RES>
C;Comment: This protein is the major nucleolar-specific protein in eukaryotic exponential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 5/3; 44/3; 211/1; 274/1; 303/1; 350/2; 392/1; 433/2; 485/1; 526/2; 571/1; 613/
C; Superfamily: nucleolin; ribonucleoprotein repeat homology
C; Keywords: DNA binding; nucleus
F;311-376/Domain: ribonucleoprotein repeat homology <RRM1>
F;371-459/Domain: ribonucleoprotein repeat homology <RRM2>
F;489-552/Domain: ribonucleoprotein repeat homology <RRM3>
F;575-639/Domain: ribonucleoprotein repeat homology <RRM3>
                                                                           Gene 68, 73-84, 1988
A,Title: Sequence and structure of the nucleolin promoter in rodents: Characterization
A,Reference number: 148118; MUID:89121496; PMID:2906027
A,Accession: 163130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- EEEEEDYEDDKDD 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEDDDDDDD----EEBEEDDSBEBVMRITPAKGKKTPAKVVPVKAKSVABEEEDDBDDBD 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISDIFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQ--ERMLRPSEWN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KSVAELKVAISELFAKN 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C34D4.14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-C4-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22885
R;Du, Z.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C34D4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSP-----EEDEEDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 KTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTKKAAVPTP--AKKAAVTPG-------KKAAATPAKKAVTPAKVVPTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 DEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 ESKKWAPPPKEVEEDSEDEEBRSEDE----DDSSGEEEVVIPOK-KGKKATTTPAKKVVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------GKKGAAQAKALVPTPGKKGA-----VTPAKGAKN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60; Mismatches 171; Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%; Score 202; DB 2; Length 712; 22.4%; Pred. No. 0.0027;
A;Cross-references: UNIPARC:UPI000017723B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVDDEDHDEGFGSEHELSENEEE-
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NiAlternate names: nucleolar protein C23
C;Species: Gallus Gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S08414; S10766; A32725; I50397; B30099
R;Maridor, G.; Niggy R.A.
Nucleic Acids Res. 18, 1286, 1990
A;Title: cDNA sequences of chicken nucleolin/C23 and NO38/B23, two major nucleolar protein
A;Reference number: S08414; MUID:90206792; PMID:2320420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Cross-references: UNIPROT:P15771; UNIPARC:UP100001308C6; EMBL:X17199; NID:g63710; PIDN:R;Maridor, G.; Krek, W.; Nigg, E.A.
                                                    R; Varmus, H.E.
submitted to the EMBL Data Library, May 1995
A; Recession: S64738
A; Molecule type: DNA
A; Residues: "MYQQ', 3-1089 <VAR>
A; Residues: "MYQQ', 3-1089 <VAR>
C; Genetics: UNIPARC: UPI0000168A23; EMBL: U20158; NID: g967212; PID: g967213
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               967 --- ERKAEBELERQFQKMMQESIDARKSEKVVASKIPVISKPVSVQKPLLLKKSBEPSSS 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 ISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQ-----NPLPSSFPGK-KITSRAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      707 INNOPNPFYLNYSDP-----PDNYFRIQLVTTILLNINRTPAAFTKKCKLLLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 PVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKT-----NMYHNEKVNFHVECKDYVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    755 -FFEYYTFIKEQPL------PKETEFRVSSTFKKYENIFGNTK-----FER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 AKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 EEDEEDVDDEDHDEGFGSEHELSENEEEEEEEBDYBDDKDDDISDTFSEPGYENDSVEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 KEVTSISSRKRGKRRYFWEYSEQLTPSQOERMLRPSEWNRDTLPSNMYQKNGLHHGKYAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 KKSRRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVSELPLTAR-----PRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           528 KE-----KNKLAF------RACRL------KKKKAQYEANKVKLWG
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.5%; Score 184; DB 2; Length 1089;
Best Local Similarity 20.2%; Pred. No. 0.04;
Matches 98; Conservative 69; Mismatches 159; Indels 160; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               947 -----RDIEMKRMYEEY------ERKLKDEE-----
                          A;Cross-references: UNIPARC:UPI000013026A; EMBL:U28158
                                                                                                                                                                                                                                                                                 A,Gene: SGD:NMD2; IFS1
A,Cross-references: SGD:S0001119; MIPS:YHR077c
A,Map position: 8R
A,Introns: 2/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-694 <MAR>
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     A;Residues: 1-1089 <LEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S08414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1084
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1099 <hr/>
A;Cross-references: UNIPROT:P38798; UNIPARC:UPI000013026A; EMBL:U14974; NID:g555938; PIL
R;Favello, T.
R;Favello, T.
A;Description: The sequence of S. cerevisiae cosmid 9205.
A;Reference number: S46795
A;Accession: S46815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;MOIecule type: DNA
A;Residues: 'MYQO',3-1089 <FAV>
A;Residues: 'MYQO',3-1089 <FAV>
A;Cross-references: UNIPARC:UPI0000168A23; EMBL:U10556; NID:g500825; PID:g500836; MIPS:X
R;Lee, S.I.; Umen, J.G.; Varmus, H.E.
Proc. Natl. Acad. Sci. U.S.A. 92, 6587-6591, 1995
A;Title: A genetic screen identifies cellular factors involved in retroviral -1 frameshi
A;Reference number: S64648; MUID:95327692; PMID:7604038
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2761 < DUZ>
A;Residues: 1-2761 < DUZ>
A;Cross-references: UNIPROT:Q18447; UNIPARC:UP1000007762A; EMBL:U58755; PIDN:AAB00699.1;
A;Experimental source: strain Bristol NZ; clone C34D4
                                                                                                                                                                                                           A;Map position: 4
A;Introns: 120/1; 201/3; 365/3; 445/2; 509/1; 728/3; 856/3; 902/3; 940/3; 1027/3; 1508/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NyAlternate names: IFSI protein; protein YHR077c
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession: S48244; S46815; S64648; S64738
R;He, F., Jacobson, A.
submitted to the EMBL Data Library, September 1994
A;Description: Identification of a novel component of the nonsense-mediated mRNA decay
A;Reference number: S48244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1668 NRH------KQHNKPAASALSRFASVKNTTPAGTPSSGGSSGGAIGKKSM 1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1712 STINLVDEROKTSGPSVASTGQAASAESLO-HOTPSL----ENLLARAMPHAFGRIAEN 1765
                                                                                                                                                                                                                                                                                                                                                                                                  170 SSFPGKKI----TSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------EDEEDVDDED---HDEGFGSEHELSENEEEEEEE 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYEDDKDDDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQERML 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEGPGSLAAGESSSLSAS-----TSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 ----VAKRQEKKG------MEPLQGHATPALPFKETQELLLSPLP-----
                                                                                                                                                                                                                                                                                   Match 5.6%; Score 188; DB 2; Length 2761; Local Similarity 22.3%; Pred. No. 0.076; les 88; Conservative 56; Mismatches 131; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 NFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DASSSAKDATTNEAQKKGGKKPKKWPKKMSSYTDV 1962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 RPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NMD2 protein - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 EEDE----
                                                                                                                                                 C,Genetics:
A,Gene: CESP:C34D4.14
                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 88
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Db 329 LSAEDMDKALQLNGKKLMGLEIKLEKAKSRESLKENKKERDARTLFVKNLPYRVTEDEMK 388 Qy 529 EKNKLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIV 575 Db 389 NVFENALEVRLVLNKEGSSKGMAYIEFKTEAREARALEKQGTEVDGRAMVIDYTGEKSQ 448 Qy 576 NRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNOVLEKTAEGNPTG 627 Db 449 QESQKGGGERESKTLIVNNLSYAASERTLQELFKKATSIKMPQNNQGRPK- 498 QS GLVGLRIPTSK 638 Qy 628 GLVGLRIPTSK 638 Db 499 GYAFVEFPTAE 509	RESULT 6 T3874 probable transcription initiation protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T38274 R;Harris, D.; Squares, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997 A;Reference number: Z21782 A;Accession: T38274 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-990 cHAR> A;Escidues: 1-990 cHAR> A;Escidues: 1-900 cHAR> A;Coss-references: UNIPROT:013936; UNIPARC:UPI000061AF2; EMBL:Z99753; PIDN:CAB16890.1; A;Experimental source: strain 972h-; cosmid c23C4 C;Genetics: A,Gene: SPDB:SPAC23C4.19 A;Map position: 1 C;Keywords: transcription initiation	Query Match 5.3%; Score 179; DB 2; Length 990; Best Local Similarity 21.1%; Pred: No. 0.064; Andels 198; Gaps 23; Matches 107; Conservative 72; Mismatches 129; Indels 198; Gaps 23; Qy 238 AKVKINPPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKE 294	LDI RGK	H & >		
Biochim. Biophys. Acta 1049, 126-133, 1990 A,Title: Structure and developmental expression of chicken nucleolin and NO38: coordinat A; Reference number: S10766; MUID:90304215; PMID:2114180 A; Accession: S10766 A; Accession: S10766 A; Accession: S10766 A; Accession: S10766 A; Accession: S10766 A; Accession: S10766 A; Accession: S10766 A; Accession: M; Doree, M; Labbe, J.C.; Nigg, B.A. Cell 60, 791-801, 1990 A; Thle: Identification of major nucleolar proteins as candidate mitotic substrates of CA; A; Accession: A32725; MUID:90182668; PMID:2178776	A; Wolecule type: protein A; Wolecule type: protein A; Wolecule type: protein A; Wolecule type: protein A; Cross references: UNIPARC:UP100001739D2; UNIPARC:UP100001739D3; UNIPARC:UP100001739D4 B; Borer, R.A.; Lehner, C.F.; Eppenberger, H.M.; Nigg, E.A. Cell 56, 379-390, 1989 A; Title: Major Nucleolar Proteins Shuttle between Nucleus and Cytoplasm. A; Reference number: 150397; MUID:89119560; PMID:2914325 A; Accession: 150397 A; Accession: 150397 A; Accession: 150397 A; Molecule type: mRNA A; Residues: 407-418,'R', 420-519,'T', 521-694 <bor> A; Residues: 407-418,'R', 420-519,'T', 521-694 <bor> A; Residues: 407-418,'R', 420-519,'T', 521-694 <bor> A; Residues: A07-418,'R', 420-519,'T', 521-694 <bor> A; Coment: Phosphorylation of this protein by GC2 kinase may contribute to the reorgani C; Superfamily: nucleolin; ribonucleoprotein repeat homology C; Keywords: DNA binding; duplication; nucleolus; nucleus; phosphoprotein; RNA binding; C; F:1-24/Domain: acidic <aci> F; 54-26Z/Region: 7-residue repeats (T-P-A-K-K-A-[A/V]) F; 524-26Z/Region: nuclear location signal F; 287-275/Region: nuclear location signal F; 283-351/Domain: Ribonucleoprotein repeat homology <rrmi> F; 283-351/Domain: RNA binding #status predicted <rnal></rnal></rrmi></aci></bor></bor></bor></bor>		117; Conservative 74 119; AEVPLSDCVQKASKPPSSTV 5 AKTPKNQMKQKKNAPPPK- 251 LLSQIHTDAAKENTCYCGAN	Db 54 AVTPAKKAATPAKKAATPAKKAVTPAKKAVATPAKKAVATPAKKAVVAPSPK 96 Qy 306 BGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSP 354 Db 97 KAAVVGKGA-KNGKNAKKEESEEBEDBDBEDBEBEBEBEBEPAVPVKPAAKKSAA 155	355	DD 216 AESEDEEDEEDEEDEEDEEDEEDEESSEDEKFVKEAPGKRKKEMANKSAPEAKKKTE 275 QY 433YFWEYSEQLTPSQQERMLRPSEWNRDTLPSNWYQKNGLHHGKYAVKKSRR 482 : : : : :

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transcription factor 1, neural - rat

N'Alternate names: neural zinc finger factor-1

C;Species: Rattus norvegicus (Norway rat)

C;Decies: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004

C;Accession: T46637

R;Jiang, Y.; Yu, V.C.; Buchholz, F.; O'Connell, S.; Rhodes, S.J.; Candeloro, C.; Xia, Y.F.

J. Biol. Chem. 271, 10723-10730, 1996

A;Title: A novel family of Cys-Cys, His-Cys zinc finger transcription factors expressed i A;Reference number: A58210; MUD:96210003; PMID:8631881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Description: binds specifically to a cis-regulatory element of the beta-retinoic acid e nervous system and in the pituitary gland C;Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P70475; UNIPARC:UPI00000E86A7; EMBL:U48809; NID:g1511631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371
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                                                                                                                                                                                                                                                                            252 DDEDDDDDDDBDEEEEEEEEPVKEAPGKRKKEMA----KQKAAPEAKKQKVEGTEPTTA 306
                                                                                                                                                                                                                                                                                                                                                                          307 FNLFVGNLNFNKSAPELKTGISDVFAKNDLAVVDVRIGMTRKFGYVDFESAEDL----EK 362
                                                     191
                                                                                                             398
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                                                                                                                                                                                                                                                                                                                                       ------WNRD-----TLPSNMYQKNGLHHGKYAVKKSRR-----TDVEDLTPNPKK 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLQI-----GNELRKINKVISDLTPVSELPLTARPRSRKEKNKLAFRACRLKKKAQYEA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 ALELTGLKVFGNEI-KLEK--------PKGKDSKKERDARTL-LAKNLPYKV 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 AKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSL
                                   ------LSENEREEEEEBDYEDDKDD
                                                                                                                                          --TKCSPEEDEED
                                                                                                                                                                                                                          DISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSE----
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309 GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1187 <JIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.0%; Score 168.5; Di
27.1%; Pred. No. 0.28;
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256 SDVVRETVDSLKLLAQGHGV-VLSENISD 283
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                                                                                                                361 EEDVDDEDHDEGFGSEHE----
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Matches 73; Conservative
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C; Function:
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A; Residues: 1-707 <SRI>
A; Residues: 1-707 <SRI>
A; Residues: 1-707 <SRI>
A; Cross-references: UNIPROT: P19338; UNIPARC: UPI0000161B7E; GB: M60858; GB: J05584; NID: g18
R; Srivastava, M.; Fleming, P.J.; Pollard, H.B.; Burns, A.L.
FEBS Lett. 250, 99-105, 1989
A; Title: Cloning and sequencing of the human nucleolin cDNA.
A; Reference number: S04631; MUID: 89290043; PMID: 2737305
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;Residues: 231-236;392,399-403;458-461;655-656,'X',658-660 <JOR>
;Cross-references: UNIPARC:UF10000177236; UNIPARC:UF1000017723D; UNIPARC:UF1000017723B;
;Experimental source: surface-labelled HeLa cells
                                                                                                                                                                  NiAlternate names: phosphoprotein pp100; protein B50; protein C23
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 09-Jul-2004
C;Accession: A35804; S04631; Ä48138; A55996
R;Srivastava, M.; McBride, O.W.; Fleming, P.J.; Pollard, H.B.; Burns, A.L.
A;Title: Genomic organization and chromosomal localization of the human nucleolin gene.
A;Reference number: A35804; MUID:90368666; PMID:2394707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site sequence r(UUAG/G) and
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R; Jordan, P.; Heid, H.; Kinzel, V.; Kuebler, D.
Biochemistry 33, 14696-14706, 1994
A; Title: Major cell surface-located protein substrates of an ecto-protein kinase are A; Reference number: A55996; MUID:95086063; PMID:7993898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------KAAATPAKKTVTPAK-- 102
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5.2%; Score 174; DB 2; Length 707;
Best Local Similarity 20.4%; Pred. No. 0.078;
Matches 99; Conservative 76; Mismatches 162; Indels 148; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA binding
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Superfamily: nucleolin; ribonucleoprotein repeat homology
;Reywords: DNA binding; nucleolus; nucleus; phosphoprotein;
;308-373/Domain: ribonucleoprotein repeat homology «RRM1>
;394-456/Domain: ribonucleoprotein repeat homology «RRM2>
;487-550/Domain: ribonucleoprotein repeat homology «RRM3>
;573-634/Domain: ribonucleoprotein repeat homology «RRM3>
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A;Cross-references: UNIPARC:UPI0000161B7E
R;Ishikawa, F; Matunis, M.J; Dreyfuss, G; Cech, T.R.
R;Ishikawa, F; Matunis, M.J; Dreyfuss, G; Cech, T.R.
Mol. Cell. Biol. 13, 4301-4310, 1993
A;Title: Nuclear proteins that bind the pre-mRNA 3' splice in A;Reference number: A48138; MUID:93309464; PMID:8321232
A;Recession: A48138
A;Molecule type: protein
A;Residues: 458-474 <ISH>
A;Residues: 458-474 <ISH>
A;Cross-references: UNIPARC:UPI0000073927
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           451
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Cross-references: GDB:125908; OMIM:164035
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        ---IRISSLITEGVNPTLDEVSKFNP
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                                                                                                                                                   nucleolin - human
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A;Cross-references: UNIPARC:UD1000053123; EMBL:Z49810; NID:g854472; PIDN:CAA89942.1; PII
A;Experimental source: strain AB972
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NyAlternate names: GARP
NyAlternate names: GARP
Species: Plasmodium falciparum
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54514
R;Triggla, T.; Stahl, H.D.; Crewther, P.E.; Silva, A.; Anders, R.F.; Kemp, D.J.
MOI Biochem. Parasitol, 31, 199-202, 1988
A;Title: Structure of a Plasmodium falciparum gene that encodes a glutamic acid-rich prot
A;Reference number: A54514; MUID:89040048; PMID:2903445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:P13816; UNIPARC:UPI00001280E0; GB:J03998; NID:g160298; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------CKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKG 278
                                                                                                                                                                                                                                                                                                                                                                                                             246 QQSRPLLSQIHTDAAKENTCYCGAV-----AKRQEKKGMEPLQGHATPALPFKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 TQELLLSPLPQEGPGSLAAGESSSLS-----ASTSVSDSSQ----KKEEHNYSLFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 EKEAKSEPQQPEDNAETAATEQVSSSNGPATDDAQATLNTDSSEANEIVKKEEG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 OFADPVVVPQSTDTKDENTSDKDTVDSGNVTTTESTERAESTSNIPPLDG-----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 NKTSEEDAQRLAKELRERYGRSSSKQYRAAAQDGYVPQRFLLPSVDTATIWGVRCRPGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 GKKITSRAAAPVCSSKTLQAEV-PLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454 GVEIINLEDKEACEEQHITVESRPLSQPQCKLIDEPEQLTLMDKSKV---EEKNLSIQEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSEHELSENEEEEEEEEDYE------VEDIXDDDISDTFSEPGYENDS-----VEDI
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                                                                                                                                                                                                                                                                                                                                                    Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 KEVTSISSRKRGK---RRYFWEYSEQLTPSQQ-----ERMLRPS------
                                                                                                                                                                                                                                                                                               Length 1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.9%; Score 165; DB 2; Length 678;
Best Local Similarity 22.3%; Pred. No. 0.22;
Matches 61; Conservative 44; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDNL---GEQPTKCS-----PEEDEEDEEDVDDEDHDEG----
                                                                                                                                                                                                                                                                                         Query Match
4.9%; Score 165.5; DB 2;
Best Local Similarity 23.2%; Pred. No. 0.36;
Matches 90; Conservative 50; Mismatches 109;
                                                                                                                 A,Cross-references: SGD:S0004470; MIPS:YML010w
A,Map position: 131
C,Keywords: nucleus; tandem repeat
F;148-216,Region: aspartic acid/glutamic acid-rich
F;931-1063/Region: 6-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 QIGNELRKLNKVISDLTPVSELPLTARP 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LIPVQELPLLKP
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C;Superfamily: histone H1
C;Keywords: tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-678 <TRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Accession: A54514
A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 YİSQKL
                                                                                            A;Gene: SGD:SPT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
                                                                 C, Genetics
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C;Superfamily: yeast peptidylprolyl isomerase FPR3; BKBP-type peptidylprolyl isomerase h
C;Keywords: nucleus; phosphoprotein
F;324-371/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
                                                                                                                       C,Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55320
R;Alnemri, E.S.; Fernandes-Alnemri, T.; Pomerenke, K.; Robertson, N.M.; Dudley, K.; DuBo J. Chem. 269, 30828-30834, 1994
A;Title: FKBP46, a novel Sf9 insect cell nuclear immunophilin that forms a protein-kinas A;Reference number: A55320; MUID:95074110; PMID:7527037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Modecule type: DNA
A; Residues: 1-1063 <SWA>
A; Residues: 1-1063 <SWA>
A; Residues: 1-1063 <SWA>
A; Cross-references: UNIPROT: P27692; UNIPARC: UPI0000053123; GB: M62882; NID: g172679; PIDN: R; Gentles, S.; Bowman, S. submitted to the EMBL Data Library, June 1995
A; Reference number: S55102
A; Accession: S55109
A; Accession: S55109
A; Modecule type: DNA
B; Residues: 1-1063 <GEN>
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N;Alternate names: protein YM9571.08; protein YML010w
C;Specias: Saccharomyces cerevisiae
C;Date: 06-Dec-1991 #text_change 09-Jul-2004
C;Accession: A40253; S55109
R;Swanson, M.S.; Malone, E.A.; Winston, F.
Mol. Cell. Biol. 11, 3009-3019, 1991
A;Tile: SPT5, an essential gene important for normal transcription in Saccharomyces (A;Reference number: A40253; MUID:91246167; PMID:1840633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | | | : : | : : | | | : EKKKPEAKK--EEAPVEKKKKQIAGGVSIEDLKVGSGPVAKAGKVVWYYYEGRLKQN-- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 SVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDE-----EDVDDEDHDEGF--- 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 -GSEHELSENEEEEEEEEDYEDDKDDDISDTFS-----EPGYENDSVEDL-KEVTSISS 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDV 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --KGP--GFKFRLGSKEVISGWD 365
                                                                                         C;Species: Spodoptera frugiperda (fall armyworm)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 QEKKGMEPLQGHATPALPFKETQEL-----LLSPLPQEGPGSLAAGESSSLSAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 EDLTPNPKKLLQIGNELRKLNKVISDLTPVSELPLTARPRSRKEKNKLAFRACRLKKKAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546 YEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.0%; Score 166.5; DB 2; Length 412; Best Local Similarity 20.6%; Pred. No. 0.099; Matches 80; Conservative 59; Mismatches 118; Indels 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 VGIAGMKVGGKRKIVCPPAMAYGAKGSP 393
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                                                                 immunophilin FKBP46 - fall armyworm
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-412 <ALN>
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	Db 910 KEKARVNYDKHKSELKPSLDKGDVVDDIIPVFAPWPALLKYKYKVKIQPGSAKKT- 964 Qy 545 QYEANKVKLWGLNTEYDNILFVINSIKQEIVNRVQNPRDERCPNWGQKLEI 595 Db 965
Qy 399 DISDTFSEPGYENDSVEDLKEVTSISSRKRGKRR 432 : :	
RESULT 12 S5252 hypothetical protein YPL009c - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein LPABc; hypothetical protein YP8132.04c C;Batesiae: Saccharomyces cerevisiae C;Bate: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004 C;Accession: S5252; S59684 R;Badcock, K.; Churcher, C. Submitted to the EMBL Data Library, February 1995 A;Reference number: S52519	C; Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004 C; Accession: T50550 R; McKeever, M.O.; Okano, H.J.; Darnell, R.B. Cell 82, 773-783, 1995 A; Title: Beta-NAP, a cerebellar degeneration antigen, is a neuron-specific vesicle coat I A; Pitle: Beta-NAP, a cerebellar degeneration antigen, is a neuron-specific vesicle coat I A; Reference number: Z25157; MUID:95401267; PMID:7671305 A; Reference number: T50650 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule v; Pype: mRN A; Residues: 1-1082 < NNEW A; Residues: 1-1082 < NNEW A; Cross-references: UNIPROT:013367; UNIPARC:UPI0000125030; EMBL:AF022152; PIDN:AAB71894.]
A; Accession: S52522 A; Molecule type: DNA A; Residues: 1-1038 < BAD> A; Cross-references: UNIPROT: 012532; UNIPARC: UPI0000552E40; EMBL: Z48483; NID: 9683777; PIL	Query Match Best Local Similarity 22.1%; Pred. No. 0.41; Matches 90; Conservative 59; Mismatches 150; Indels 109; Gaps 17;
	Qy 176 KITSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNF 227
A; Reference number: \$59677 A; Accession: \$59684 A; Accession: \$59684 A; Residues: 1-1038 < HAL> A; Residues: 1-1038 < HAL> A; Cross-references: UNIPARC: UPI000052E40; EMBL: U33335; NID: 9965076; PID: 9965084; MIPS: Y C; Genetics:	Qy 228 HVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGA 269 :: : :
A;Cross-references: SGD:S0005930 A;Map position: 16L	595 LSRHAKKLFLAPKPAPVLESSFKDRDHPQLGSLSHLINAKATGYQELPDWÞERÞD-
Query Match 4.9%; Score 165; DB 2; Length 1038; Best Local Similarity 20.8%; Pred. No. 0.37; Matches 103; Conservative 73; Mismatches 175; Indels 144; Gaps 21;	Qy 311 LAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDEDHD 370
Qy 201 VQKASKPPSSTQIMVKTINMYHNEKVNFHVECKDYVKKÄKVKINPVQQSRPLLS 253	OY 371 E-GFGSEHELSENEEEEEEEFDYEDDKODDISDTFSEPGYENDSVEDLKEVT 421
Qy 254 QIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGS 310 : :	QY 422 SISSRKRGKRYFWEYSEQLIPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSR 481
Qy 311 LAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEDVDDEDHD 370	QY 482 RIDVEDLIPNPKKLLQIGNELRKLNKVISDLIPVS 516
Qy 371 EGFGSEHELSENEEBEEBEDYEDDXDDDISDTFSEBGYENDSVE-DLKE 419	RESULT 14 S2286 NA FORMISCHETSE (RC 5, 99,1,2) I - Arabidonsis thaliana
Qy 420YYFWEYS 438 : : : : : : : :	use-ear cression 13-Jan-19
QY 439 EQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTP 490	R;Atteber, J.K.; Signer, E.K. Submitted to the EMBL Data Library, September 1990 A;Description: Cloning and characterization of an Arabidopsis TOP1 gene. A;Reference number: S22864
491	A;Accession: S22864 A;Molecule type: mRNA A;Residues: 1-916 <kie></kie>

A,Gene: SGD:NAB3; NAB3; HMD1; MIPS:YPL190c A,Cross-references: SGD:S0006111

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A; Experimental source: strain S288C (AB972)
R; Sugimoto, K.; Matsumoto, K.; Kornberg, R.D.; Reed, S.I.; Wittenberg, C.
Mol. Gen. Genet. 248, 712-718, 1995
A; Title: Dosage suppressors of the dominant GI cyclin mutant CLN3-2: identification of A; Reference number: S60122; MUID:96069710; PMID:7476874
                                                                                                                                       A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-340,'I',342-802 <SUG>
A;Cross-references: UNIPARC:UPI0000694F8; GB:D37935; NID:g1235749; PID:g1235750
C;Genetics:
               A,Cross-references: UNIPROT:P30181; UNIPARC:UPI000013712B; EMBL:X57544; NID:g16557; PID:
                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                   61 VTSPNGTIPSNKTSIVKSSMPSSSSKASPAKSPLRNDMPSTVKDRSQLQ------ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 KVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 -RASRIIKDESDDETPISSMFRKKIDSGMSGGNQLSNDEKKPLVQKLHQNGSTVKNEVPN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 GKV-----LGKRPLEKNSSADQSSLKKAKISASPTSVKMKQDSVKKEIDDKGRVLVSPKM 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENEREEEEEDYEDDKDDD--ISDTF-SEPGYENDSVEDLKEV--TSISSRKRGKRRYFW 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 HGK------YAVKKSRRTDV-----EDLTPNPKKLLQIGNELRKLNKVIS 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLTPVSELPLTARPRSRK--EKNKLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVIN 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494
                                                                                                                                                                                                                                                                 111 GTKEVDYLGLDDFSSPYQDEEVIS--KTPTLAQLNSEDSQSVSD-SLYYPDSLFSVKQNP 167
                                                                                                                                                                                                                                                                                                                                                               168 LPS---SFPGKKIT-SRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYSEQLIPSQQERMLRPSEWNRD------TLPSN-----MYQKNG---LH 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : : | | : : | : : | : : 335 SPRSRAMTKNTKUTKUSKYSTSSKSSPSSGDGQKKWTTLVHNGVIFPPPYKPHGIKILY 394
                                                                                                                                                                                                                                                                                                2 GTETVSKPVMDNGSGDSDDDKPLAFKRNNTVAS-NSNQSKSNSQRSKAVPTTKVSPMRSP 60
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DPTPIYEWHLEEKEKKKQMSTEEKKALKGERMKQEEKY------MWA------VVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 GHATPALPFKETQELLLSPL-----PQEGPGSLAAGESSSLSASTSVSDSSQKKEEHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----CSPEEDEEDVDDEDHDEGFGSEHELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 KAKQLSTREDGTDDDDDDDVPISKRFKSDSSNSNTSSAKPKAVKLNSTSSAAKPKARNVV
                                                                                                                                                                                                                 Gaps
                                                                                                                                                              Query Match
4.9%; Score 164; DB 2; Length 916;
Best Local Similarity 21.1%; Pred. No. 0.35;
Matches 124; Conservative 98; Mismatches 226; Indels 140;
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C;Keywords: DNA binding; DNA replication; isomerase
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                                                               A;Gene: TOP1
C;Superfamily:
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NAB3 protein - yeast (Saccharomyces cerevisiae)

NAB4 protein - yeast (Saccharomyces cerevisiae)

NyAlternate names: probable RNA/ssDNA-binding protein HMD1; protein P1945; protein YPL19

C;Species: Saccharomyces cerevisiae

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: S48529; 865209; 650122

R;Wilson, S.M.; Oberdorf, A.M.; Datar, K.V.; Swedlow, J.R.; Paddy, M.R.; Swanson, M.S.

submitted to the EMBL Data Library, January 1994

A;Pserfering in Characterization of Nuclear Polyadenylated RNA-Binding Proteins from Sacc

A;Accession: S48529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: DNA
A,Residues: 1-802 <MIL>
A,Ectidues: 1-802 <MIL>
A,Cross-references: UNIPROT: P38996; UNIPARC: UPI000004F979; EMBL: U05314; NID: 9476219; PID
R;Rieger, M.; Mueller-Auer, S.; Schaefer, M.
R;Rieger, M.; Mueller-Auer, S.; Schaefer, M.
A;Reference number: 865202
A;Accession: 855209
RESULT 15
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Molecule type: DNA Residues: 1-802 <RIE> Cross-references: UNIPARC:UP1000004F979; EMBL:Z73546; NID:g1370396; PID:g1370397; GSPD

14; 385 ---EDLKEVTSISSRKR 428 168 488 210 524 211 LOKQVKYIMDSNMLNLPQFQHLPQEEKMSAILAMLNSNSDTALSVPPHDSTISTTASASA 270 271 TSGARŚNDQRKPPLSDAQRRMRFPRADĽSKPITEEEHDRYAAYLHGENKITEMHNIPPKS 330 331 KKEEHNYSLFVSDNLGEQPTKCSPEEDEE-----DEEDVDDEDHDEGFGSEHELSENEEE 429 GKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDL 489 TPNPKKLLQIGNEL------RKLNKVISDLTPVSELPLTARP------525 ----RSRKEK-----NKLAFRACRLKK---KAQYEANKVKLWGLN-TEYDNL----Gaps A;Map position: 16L C;Superfamily: yeast NAB3 protein; ribonucleoprotein repeat homology C;Keywords: nucleus; RNA binding F;331-396/Domain: ribonucleoprotein repeat homology <RRM1> 66 331 RLFIGNLPLKAVSKEDLFRIFSP-----YGHIMQINIKNAFG 367 -LFV----INSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLG 602 Query Match 4.9%; Score 163.5; DB 1; Length Best Local Similarity 22.1%; Pred. No. 0.32; Matches 76; Conservative 57; Mismatches 112; Indels EEEEEDYEDDKDDDISD----TPSEPGYENDSV----386 169 셤 ઠે ద 임 셤 ð ద ð ઠે ò

Search completed: February 28, 2006, 08:54:17 Job time : 41.9699 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

February 28, 2006, 08:45:31; Search time 234.353 Seconds Run on:

(without alignments)
1923.730 Million cell updates/sec

Title: Perfect score:

US-10-717-665A-44 3349 1 MPQPSVSGMDPPFGDAFRSH......TAEGNPTGGLVGLRIPTSKV 639 Sequence:

BLOSUM62 Scoring table: 2166443 seqs, 705528306 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot_sprot:* 2: uniprot_trembl:* UniProt 05.80:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	9	Query	1 1 1 1	0	£	Description
. i	score	Match		9 ;	1.0	Description
п	3328	99.4	639	7	Q8IUR6_HUMAN	homo
7	3326	99.3	639	~	Q81ZG1_HUMAN	homo
e	3136.5	93.7	640	7	Q8CDG5_MOUSE	
4	3129	93.4	604	N	QSHYKO_HUMAN	homo
S	2148	64.1	408	7	QSHYG4 HUMAN	homo
9	2148	64.1	417	7	Q86YR3_HUMAN	homo
7	1704.5	50.9	351	α	Q8C8N7_MOUSE	Q8c8n7 mus musculu
8	1602.5	47.9	330	~	Q9CTQ7 MOUSE	_
σ	1377.5	41.1	900	~	Q4RRX3 TETNG	
10	959	19.6	131	7	Q5ZMD5_CHICK	
11	417	12.5	755	~	Q9VC61 DROME	
12	386	11.5	293	7	Q7QG21_ANOGA	
13	227	6.8	2649	~	Q7RAS7_PLAYO	_
14	212	6.3	191	7	Q7RBX2_PLAYO	plas
15	210	6.3	707	7	Q8CE30_MOUSE	mus
16	209	6.2	106	н	NUCL MOUSE	BUM
17	209	6.2	707	~	Q99K50_MOUSE	mus
18	209	6.2	707	~	Q548M9_MOUSE	mus
19	208	6.2	444	~	Q9CT46 MOUSE	Q9ct46 mus musculu
20	208	6.2	707	~	Q8CD23_MOUSE	_
21	205	6.1	628	7	Q4Y1E8 PLACH	Q4yle8 plasmodium
22	204.5	6.1	1852	7	Q9C2H4 NEUCR	
23	. 204	6.1	1182	7	Q8ID30_PLAF7	
24	202	6.0	712	Н	NUCL RAT	
25	201	6.0	919	7	Q81510 PLAF7	
26	199.5	6.0	734	7	Q8IDC4_PLAF7	Q8idc4 plasmodium
27	197.5		714	7	QSU328_RAT	• •
28	196.5	5.9	1162	7	Q98148_HHV8	
29	195.5		771	7		-
30	195	5.8	1708	~	Q8I413_PLAF7	
31	195	5.8	2694	7	Q7RDP5_PLAYO	Q7rdp5 plasmodium

Q9dun0 human herpe Q911x9 human herpe Q813t6 plasmodium Q8f2j8 leptospira Q9g71 human herpe Q7rkz2 plasmodium Q96mu7 homo sapien G7394 narke japon Q81kh9 plasmodium Q18447 caenorhabdi Q7rth1 plasmodium Q7rth1 plasmodium Q7rth1 plasmodium Q7rth1 plasmodium Q7rth1 plasmodium Q7rth1 plasmodium Q7rth1 plasmodium Q7rth1 plasmodium Q76997 caenorhabdi Q740947 human herpe Q54094 dictyosteli Q54098 schistosoma
Q9DUNO_HHV8 Q91LX9_HHV8 Q813T6_PLAF7 Q813T6_PLAF7 Q812J1_HHV8 Q78X22_PLAYO Q78X22_PLAYO Q78X22_PLAYO Q7784_NARJA Q81KH9_PLAF7 Q18447_CAEEL Q18447_CAEEL Q18447_CAEEL Q544P8 Q544P8 Q544P8 Q544P8
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194.5 194.5 194.5 193.5 191.5 189.5 188 188 188 187.5 187.5

ALIGNMENTS

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TISSUB-Lung;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hashe F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Robak S.A., McEwan R.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Balberterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Balberterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Brownstein M., Schein J.E., Jones S.J.M., Marra M.A.;

Rodersation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung;
Director MGC Project;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC041709; AAH41709.1; -; mRNA.
Ensembl; ENSG0000164463; Homo sapiens.
InterPro; IPR00487; TF DZIP.
PROSITE; PS00036; BZIP BASIC; UNKNOWN 1.
SEQUENCE 639 AA; 72118 MW; ECFB92D9290DEDEB CRC64;
                                                                                                     Last sequence update)
Last annotation update)
                                       639 AA
                                       PRT;
                                                                                 Created)
                                     QBIURG_HUMAN PRELIMINARY;
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                                                                               01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                               Adult retina protein.
Name=LOC153222;
                                                                                                                                                                                            Homo sapiens (Human)
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Length 639; Indels Ouery Match
99.4%; Score 3328; DB 2;
Best Local Similarity 99.5%; Pred. No. 1.4e-148;
Matches 636; Conservative 0; Mismatches 3;

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Gaps ö

1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL 60

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SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE-Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.101
Carninci P., Hayashizaki Y.;
Hayashizaki Y.;
Mith-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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NUCLEOTIDE SEQUENCE.
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Name=A930001N09Rik;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mault-retina protein.
Homo sapiens (Human)
Bukaryota; Metazoa Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL
                                                                                                                 AAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV
                                                                                                                                                                     KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL
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SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL
                                          SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL
                                                                          DDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSR
                                                                                    DDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSR
                                                                                                                                     AAAPVCSSKTLQAEVPLSDCVQKASKPTSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV
                                                                                                                                                          KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL
                                                                                                                                                                                                   SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEED
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                                                                                                                                                                                                                                                         TSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKS
                                                                                                                                                                                                                                                                                                                              RRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVSELPLTARPRSRKEKNKLAFRACRL
                                                                                                                                                                                                                                                                                                                                                                       KKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDT
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WICLEOTIDE SEQUENCE.

Li F., Yao K.T.;

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY139008; AAN28956.1; -; mRNA.

InterPro.; IPR004827; TF_bZIP.

PROSITE; PS00036; BZIP BASIC; UNKNOWN 1.

PROSITE; PS00036; BZIP BASIC;

TOTAL
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QBIZGI;
01-MAR-2003 (TrEMBLrel. 23
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4932441F15 product:hypothetical protein, full insert
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STRAIN=C57BL/61; TISSUE=Testis;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
Thanlysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kahil P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T., Bakai K., Okido T., Furuno M., Ano H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., A. Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamcto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storck K.-F., Whinmay L., Mynhaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S., Langachi V., Langachi V., Kawaji H., Kohteuki S.,
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R EBBL, AKO30092; BAC26779.1; - MRNA.
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STRAINE-C578L/GJ. TISSUB-Testis;

MEDILINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100.

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,

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BREATIN-CSTBL/64): TISSUE-Testis;

BRIDINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;

BRIDINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;

BRIDINE AKIYAMA J., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Yamamoto R., Matsunca S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunco H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ogawa K., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramateu M., Inohe Y., Kira A., Hayashizaki Y.;

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                                                                                                                                                                                                                                                                                                              Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Pred. No. 1.4e-139;
19; Mismatches 22;
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PROSITE; PS00036; BZIP_BASIC; UNKNOWN_1.
Hypothetical protein.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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The German CDNA CONSORTIUM;
Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX647573; CAI46104.1; -; mRNA.
InterPro; IPR004627; TF bZIP.
PROSITE; PS00036; BZIP_BASIC; UNKNOWN_1.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypotheital protein DKFZp313F2319 (Fragment)
Name=DKFZp313F2319;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein DKFZp686G2059 (Fragment).
Name=DKFZp686G2059;
            Score 3129; DB 2;
Pred. No. 2.9e-139;
     93.0%; Pred. No. 2...
2; Mismatches
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The German cDNA Consortium;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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Hypothetical protein.
SEQUENCE 417 AA; 46579 MW; 9DBD37B07C14556B CRC64;
45625 MW; E3E36BFEA8B4284B CRC64;
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99.8%; Pred. No. 2.4e-93;
iive 0; Mismatches 1;
                                          64.1%; Score 2148; DB 2; 99.8%; Pred. No. 2.4e-93;
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NETLINE-257BL/62; TISSUB-Retina;

NETLINE-257BL/62; TISSUB-Retina;

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NETLINE-257BL/62; TISSUB-Retina;

NETLINE-257BL/62; TISSUB-Retina;

NETLINE-257BL/62; TISSUB-Retina;

NETLINE-257BL/62; TISSUB-Retina;

NETLINE-257BL/62; TISBUB H., Rondo B., Furbuda S.,

NA Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Gasavant T.,

NA Fleischmann W., Gasaterland T., Gissi C., King B., Kochiwa H.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Gasavant T.,

Nathl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baddarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Bronnersin M.J., Bult C., Pletcher C., Fullia M., Mazianelli J., Nombaerts P.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Nombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald M., Weditucz I., Sakamoto N.,

Sanzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nordone P., Wang K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nordone P., Nambaw-Bootis A., Yoshida K., Rawaji H., Kohtsuki S.,

Nordone P., Wang K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nordone P., Wang R., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nordone P., Wang R., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nordone P., Wang R., Wang K., Wang W., Kawaji H., Kohtsuki S.,
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The PANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                  AAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV
                                                                                                        KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930040G19 product:hypothetical protein, full insert sequence.
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C55BL/6J; TISSUE=Retina; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                 MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama T., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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Ensembl; ENSMUSG0000048249; Mus musculus.
MGI; MGI:1924378; A930001N09Rik.
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KRAIN-CSTBL/60; TISSUE-Retina;

KRANIN-CSTBL/60; TISSUE-Retina;

KRANIN-CSTBL/60; TISSUE-Retina;

KRANIN-CSTBL/60; TISSUE-Retina;

KRANIN-CSTBL/60; TISSUE-Retina;

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A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Kato T., Kato T., Kato T., Kato T., Kato T., Kato T.,

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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

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Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sakai H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

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Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930001N09 product:hypothetical protein, full insert sequence.
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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"Functional annotation of a full-length mouse cDNA collection.";
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STRAIN=C57BL/6J; TISSUE=Retina;
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Q9CTQ7;
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Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konuo H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AKO20796; BAB32214.1; -; mRNA.
BRBL, AKO20796; BAB32214.1; -; mRNA.
BRBL, AKO20796; BAB32214.1; -; mRNA.
M. HOCHICAL IDIOCHALIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPPSSFPSKKIÍN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 RAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAK
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Herradontoidea, Tetraodontidae, Tetraodontidae, Tetraodontillae, Tetraodontillae, 11]
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Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kaw
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIXRN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.9%; Score 1602.5; DB 2; Length 92.7%; Pred. No. 8e-68; cive 8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 AA; 36692 MW; 1397555C4934A64B CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 7 SCAF15001, whole genome shotgun sequence.
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13-SEP-2005 (TrEMBLrel. 31, Last seq
13-SEP-2005 (TrEMBLrel. 31, Last ann
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Q4RRX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 306; Conservative
                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
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19.6%; Score 656; DB 2; Length 131; 90.1%; Pred. No. 8.5e-24; ive 6; Mismatches 7; Indels
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O9VC61, 08T9A9;
01-MAY-2000 (TERMELrel. 13, Created)
01-MAR-2003 (TERMELrel. 23, Last sequence update)
10-MAY-2005 (TERMELrel. 30, Last annotation update)
CG13624-PA, isoform A (CG13624-Pb, isoform b) (SD09792p)
ORFNAMMES=CG13624;
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Last sequence update)
Last annotation update)
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25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
ORFNames=RCJMB04_2h14
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Matches 118; Conserv
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             Andread S., Jaffe D., Fisher S., Journal D., Stange-Thomann N., Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Macaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B., Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B., Anthouard C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Relis M., Volff J., Chapple C., McKernan K.J., McEwan P., Bosak S., Arlis M., Volff JM., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Mincker P., Lander E.S., Weissenbach J., Roest Crollius H., Genome duplication in the teleost fish Tetraodon nigroviridis reveals I. Nature 431:946-957(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNPLPSSFPGKKITSRAAAPVCSSK------T-T-CAEVPLSDCV---QKA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 SKP-PSSTQIMVKTNMYHNEKVNFHVECKDYVK-KAKVKINPVQQSRPLLSQIHTDAAKE 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 STSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHELSE 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 NEEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKEVTS-ISSRKRGKRRYFWEYSEQ 440
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OUTCOING Whitehead Institute Centre for Genome Research;
Genoscope; Whitehead Institute Centre for Genoscope;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
41.1%; Score 1377.5; DB 2; Length 600;
Best Local Similarity 43.8%; Pred. No. 5.9e-57;
Matches 316; Conservative 74; Mismatches 126; Indels 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600 AA; 66291 MW; B2F28B2F3B27B1C4 CRC64;
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540 RKVNDVNVDLKYILKHFSLSPQVAPPVAGQTSDFVNKILDNTGRGDPTGGLVGLRVPTSK 599 61 SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL 120 1 MPQPSVSGMDPPFGDAFRSHVFSEQTLMSTDLLASSSDPDFMYELDREMDYQQSSRDNLL 1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL ----LPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSK NUCLEOTIDE SEQUENCE. MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gaps Caldwell R. B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J., Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M., Plachy J., Carninci P., Hayashizaki Y., Buersetedde J.M.; Fill-length cDNAs from chicken bursal lymphocytes to facilitate genefunction analysis.; Genome Biol. 6:R6-R6(2005).

EMBL; AJ719449; CAG31108.1; -; mRNA. ö Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

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Amanatidae N.D., Calliber S.E., B.I. R.A., Thostins R.A., Callib R.P.,
Amanatidae G.G., Scherz S.E., Ell R.A., Hostins R.A., Callib R.P.,
Sutton G.G., Worthan D. R., Yandad S., Ashunrar K. Henderson S.M.,
Burndon R.C., Negers Y.-H.C., Chame, M. Pfeidfer B.D.,
Amanatidae R.C., Morthan J.R., Yandall W.D., Zhang O., Chen L.Y.,
A. Barton R.C., Morthan J.R., Yandall W.D., Zhang O., Chen L.Y.,
A. Barton R.C., Morthan J. A., And J. A., Anderser-fatantoon C., Baldarin D.,
Barton G.G., Barter E.G., Halt G., Nalaon C.R., Miklos G.L.G.,
A. Barton R.M., Essu A. A., Barton B. J., Barton C.R., Miklos G.L.G.,
Beaten R.M., Cand B. B., Balcher A., Deng Z., Mays A.D., Dew J.D., Davies D. B.
Burtlas K.C., Dusan D. A., Buller B.C., Deverders P. Bartis R.M.,
Burtlas K.C., Dusan D. A., Buller B.C., Gaden E., Center J., Chartes J.M.,
Burtlas K., Davies D., Balcher A., Deng Z., Mays A.D., Dew J.D., Dew J.D., Davies D.,
Burtlas K., Davies D., Balcher A., Deng Z., Mays A.D., Dew J.D., De
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133 ---ISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSF-PGKKITSRAAAPVCSS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 QEGPGSLAAGESSSLSASTSVSDSSQXKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 SSNGIGSGSGGYFTPDMSHSLSLANVVSEQVLLQEATTFN------ELLYEMTPNSNAMW 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 DIYCEDLIKYIKLISCDIWGIKEVDYL----GLDDFSSP-----YQDEEV-- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---IEDFLPQTAV-----TQSVNFLLSPQAQGQDALVAPPMELLQQQQQNHQQLQVGS 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 VQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 510 -----LĞLEHIWMRREPRQHLLSTGSLAEAESFSSLSTGSVLSPDGIDFSQDDEDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562 SSENSDNYDDCSSDNGLSEDEDETRISTENHILSSSKGKERFFWQYNVQAKGPKGRKLVFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 ----RPSEWNRDTLP-----SNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 LPQLQTLLTLSQQQQSNSSSTSPYEIYHSTPQKPQQQQLSASPSPGSQASQSPLTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 KTLQAEVPLSDCVQKASKPPSST----QIMVKTNMYHNEKVNFHVECKDYVKKAKVKINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 DDEDHDEGFGSEH------ELSENEE-------EESEEBDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 EDDKDDDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQERML--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----CKDIENLE--SFTDVLDNEGALTSNWEQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 SDISSAIIHTKHEPFSLDDDYIFPNDKAEIQAADLSDLNGGDFLDVIGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461 SSGFGSSASGNSTTTSNOTS---GSAVRKSFGYQSAVENSQLSRLSSSAPTH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 SVSGMDPPFGDAF---RSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL-
                                                                                                                                                                                                                                   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawpe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC.2001) to the EMBL/GenBank/DDBJ databases.
     Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 240;
                                                                                                                                                                                                                                                                                                                                                 12.5%; Score 417; DB 2; Length 755;
                                                                                                                                                                                 Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                      "Drosophila melanogaster release 4 sequence."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                           IntAct; Q9VC61; --
Ensembl; CG13624; Drosophila melanogaster.
Flyaase; FBgn0039209; CG13624.
InterPro; IPRO04827; TF bZIP.
PROSITE; PSS00036; BZIP BASIC; UNKNOWN 1.
SEQUENCE 755 AA; 82263 MW; D851D42235FF10E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81; Mismatches 183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.1%;
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Matches 160; Conservative
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                              NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           464 MYQKN----GLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVSELP 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 ENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQERML-----RPSEWNRDTLPSN 463
            556
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                       673 NIGKELDKLSRTINDMIPVSELPPNVRPKSRKEKNKLASRACRLKKKAQHEANKIKLFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAAGTTSAAVSVGSNAGTSGTAMSRLSSSAPTHISGFEQIWQRREPRPHLLSTGSLAEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 TKCSPEEDEEDEEDVDDEDHDEGFGSEHELSENEEEEEEEEDVEDDKDDDISDTFSEPGY
          QIGNELRKLNKVISDLTPVSELPLTARPRSRKEKNKLAFRACRLKKKAQYEANKVKLWGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62; Gaps
                                                                                                                                                                                                            Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
                                                                                                                                                                                                                                                                                                                                                   The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBI/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%; Score 386; DB 2; Length 293; 36.3%; Pred. No. 1e-10; ative 38; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                  "Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  520 LTARPRSRKEKNKLAFRACRLKKKAQYEANKVKLWGLNTEY 560
                                                                                                                                              01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGPO0000015170 (Fragment).
ORFNames=ENSANGG0000012681;
                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.

EMBL; AAAB01008844; EAA06118.2; -; Genomic_DNA.

GO; GO:0005634; C:nucleus; IEA.

InterPro; IPR004827; TF_DZIP.
                                                                                                                                                                                                                                                                                    The Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00036; BZIP BASIC; UNKNOWN 1.
                                                                                                                                                                                                    Anopheles gambiae str. PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 36.3%
Matches 102; Conservative
                                                                                                                            Q7QG21_ANOGA PRELIMINARY;
                                                                                                                                                                                                                                   Anophelinae; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                     557 NTEY 560
                                                                         EIEH 736
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51 YQQNPRD----NFLSLEDCKDIENLESFIDVLDNEGALTSNWEQWDTYCEDLTKYTKLTS 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 LKKNNPDDATKHFWKPKTFKDINGLYYDT----NEKAIDIDLLKWEH--EKLTRMSSLTN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDIWGTKEVDYLGLDDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQN 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 BOPTKCSPEEDEEDEDVDDEDHDEGFGSEHELSENEEEE-EEEEDYEDDKDDDISDTFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22255706; PubMed=12368865; DOI=10.1038/nature01099; Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Perterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates J.R. III, Rains J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
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Best Local Similarity 19.0%; Pred. No. 0.037;
Matches 131; Conservative 110; Mismatches 188; Indels 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/Gebank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                        Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.

EMBL; AABL01002172; EAA18637.1; -; Genomic_DNA.
InterPro; IPR011591; Botulinum.
Probom, P001963; Botulinum; 2.
Hypothetical protein.
SEQUENCE 2649 AA; 309810 MW; E7207F344643AC24 CRC64;
                                                                                                           Last sequence update)
Last annotation update)
             2649 AA
                                                                            Created)
                                                                        01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein.
QTRAST_PLAYO PRELIMINARY;
Q7RAS7;
                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=73239;
                                                                                                                                                                                                                Name=PY06422;
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8 8 8 8 8 8 8	Db Qy Qy Bb Bb Bb Bb Bb Bb Bb Bb Bb Bb Bb Bb Bb	94 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	R R R R R R R R R R R R R R R R R R R	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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.4. 402 LSFNITEDELKEVFEDAMEIRLVSQDGKSKGIAYI--EFKSE-ADAEKNLEEKQGAEIDG 458
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                                                                                                        NUCLEOTIDE SEQUENCE.
STRAINE-STBL/61; IISSUE-Skin;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I all Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUB=Skin; MBDLINB=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.; Nuramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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STRAIN=C57BL/6J; TISSUG=Skin;
MTEDLIND=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,
Vamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Voneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kashiwai K.,
Voneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai Jf.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
"RIEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.",
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21.0%; Pred. No. 0.053;
ative 78; Mismatches 180; Indels 224; Gaps
   "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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MGI; MGI:97286; NCl.
GO; GO:0005730; Crnucleolus; TAS.
InterPro; IPR012677; a b plait nuc_bd.
InterPro; IPR0005604; NNPl_RNA_bd.
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The invention relates to a method of determining the angiogenic index of a tissue or cell sample comprising assessing, in a sample, the expression trevals of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the angiogenic index. The methods and compositions of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the angiogenic index of a tissue or cell sample using expression levels of differentially expressed genes, useful for diagnosing or treating cancer, coronary artery disease, myocardial ischemia and/or arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 23; SEQ ID NO 44; 296pp; English.
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25	26	27	78	29	30	31	32	33	34	35	36	37	38	39	40	41	4	4.4	44	24.5	

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cytostatic; cardiant; vasotropic; antiarteriosclerotic; angiogenesis inhibitor; angiogenesis stimulator; angiogenesis stimulator; angiogenesis setimulator; angiogenes; conex; gene expression; cancer; coronary artery disease; myocardial ischemia; coronary arteriosclerosis; forensic medicine.
                                                                                                                                                                                Angiogenesis-differentially expressed protein ANH0757.
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ADK65805 standard; protein; 639 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2002; 2002US-00067482.
10-JUN-2002; 2002US-00164595.
16-AUG-2002; 2002US-0403649P.
03-JAN-2003; 2003US-0437746P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2003; 2003WO-US003848
                                                                                                                            06-MAY-2004 (first entry)
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Human PRO Human PRO Human PRO

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Membrane

EP1440981-A2

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invention are useful for diagnosing, preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary arteriosclerosis. They can also be used in research, drug discovery and forensic medicine involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention.
                                                                                                                                                                                                                                                                                                     DDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDT
                                                                                                                                                                                                                                                                                                                                                             AAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 RRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVSELPLTARPRSRKEKNKLAFRACRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDT
                                                                                                                                                                       1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL
                                                                                                                                                                                                 1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL
                                                                                                                                                                                                                              SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL
                                                                                                                                                                                                                                                       SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL
                                                                                                                                                                                                                                                                                      DDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSR
                                                                                                                                                                                                                                                                                                                                            AAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKS
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                                                                                                               ; Score 639; DB
; Pred. No. 0;
0; Mismatches
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                                                                                                                                           639; Conservative
                                                                                                                              Similarity
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                                                                                                               Query Match
Best Local 8
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The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% to 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a protein sequence of the invention.

Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers

Claim 1; SEQ ID NO 3633; 2449pp; English.

ŝ Ishii

Sato H,

Wakamatsu A,

Irie R;

Otsuki T, Nagai K, I

Sugiyama T, Isono Y,

Yamamoto J,

Isogai T,

2004-535376/52. N-PSDB; ADQ64284.

(REAS-) RES ASSOC BIOTECHNOLOGY 21-JAN-2003; 2003JP-00102206. 09-MAY-2003; 2003JP-00131392. 21-JAN-2004; 2004EP-00001196

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                                                                                                                                                                                                                                                                                                                                                            8; Length 417;
                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                           48.0%; Score 307; DB 8;
99.8%; Pred. No. 4e-290;
tive 0; Mismatches
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Matches 407; Conservative
                                                                                                                                                                                                                                                                                                                                        Sequence 417 AA;
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osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic, gene therapy, diagnostic marker, morbid state, osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia,

Homo sapiens

Novel human protein sequence #1445

07-OCT-2004

ADQ66472;

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This invention relates to a novel isolated polynucleotide comprising a nucleotide sequence selected from one of 1680 sequences, a mature protein coding portion of them, an active domain of them and their complementary sequences. The invention may be useful for the production of compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with an antiatthritic, antiparkinsonian, neuroprotective, nootropic, immunosuppressive, cytostatic, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal, antiparal,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polynucleotide encoding bone marrow derived polypeptides useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "OTHER= All Xaa's in this sequence are unknown amino acids or the site of a stop codon within the DNA sequence"
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                                                                                                                                                                          immunosuppressive; cytostatic; antipsoriatic; antiinflammatory; antibacterial; antiviral; antifungal; antiparasitic; gene therapy; arthritie; Parkinson's; Alzheimer's; autoimmune disease; cancer; psoriasis; inflammatory bowel disease; infection; bacteria; virus;
                                                                                                                                                antiarthritic; antiparkinsonian; neuroprotective; nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 8017; 504pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treating, e.g., Parkinson's, Alzheim
disease, and inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                     Novel human polypeptide SeqID8017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .256
/label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAR-2000; 2000US-00519705.
19-MAY-2000; 2000US-00574454.
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                          06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                          fungus; parasite; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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The present invention relates to novel human coding sequences (ABQ99268-CC ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in therefield of molecular biology as hybridisation probes, primers for used in the field of molecular biology as hybridisation probes, primers for protein, or in generation of anti-sense DNA or RNA. The polymucleotides are useful in diagnostics as expressed sequence tags (ESTS) for identifying expressed genes or for physical mapping of the human genome. The proteins may be used as molecular weight markers, or as nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or pluripotential state.

CC sequil for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals or the development of bio-sensors. The polymuclocides and proteins are useful for preventing, treating or ameliorating disorders involving aberrant protein expression or biological activity, e.g. haematopoietic disorders, central/peripheral curvical, bacterial or fungal infection, autoimmume disorders, allergic reactions and conditions, coagulation wite assembled from ESTS collated mainly by sequencing by hybridisation, and in some cases, collated mainly by sequencing by hybridisation, and in some cases, collated mainly by sequencing by hybridisation, and in some cases, collated mainly by sequencing by hybridisation, and in some cases, collated mainly by sequencing by hybridisation, and in some cases, collated mainly by sequencing by hybridisation, and in some cases, collated mainly by sequencing by hybridisation, and in some cases, collated mainly by sequencing by hybridisation, and in some cases, collated mainly by sequencing by hybridisation, and in some cases.
                                                                                                                                                                                                                                                                                                                                                   Human, expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; antionimume disorder; coagulation disorder; nootropic; antiallergic; antiinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V, Zhang J, Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V
Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 588; 394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunostimulant; cerebroprotective.
                                                                                                                                                                   ABP64928 standard; protein; 168 AA.
                         231 EEDYEDDKODDISDTFSEPG 250
  EEDYEDDKDDDISDTFSEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-NOV-2001; 2001WO-US042950.
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                                                                                                                                                                                                                                                                25-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                              Human protein SEQ ID 588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-590824/63.
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389
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mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                    Sequence 296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ORIG-) ORIGENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003066831-A2
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                                                             invention
                                                                                                                                                                                                                                                                                                                                                                     226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADK65836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
ADK65836
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                                                                                                                                                                                                      61 QEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome; vasculitis, sarcoidosis, autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis, diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders in mammals. The immune arthritis, osteoarthritis, juvenile chronic arthritis, systemic arthritis, systemic solores, as arthritis, systemic shapes arthritis, systemic shapes arthritis, and arthritis, and arthritis, and arthritis, and arthritis, and arthritis, and arthritis, and arthritis, and arthritis, diabetes haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
                                                                                                                                                       1 MVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKR
                                                                                                                                                                                      274 QEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKE
                                                                                                                              214 MVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKR
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; PRO; immune related disorder; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM; Wu TD;
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                                                                          Length 168;
                                                                                                                                                                                                                                                          EHNYSLFVSDNLGEQPTKCSPEEDEEDVDDEDHDEGFGSEH 377
                                                                                                   0; Indels
  was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                          DB 5; Le
5.4e-151;
                                                                       25.7%; Score 164; DB
100.0%; Pred. No. 5.4
cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                          ADO20373 standard; protein; 296 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2003; 2003WO-US035268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-2002; 2002US-0425235P.
                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO polypeptide #633
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                   Matches 164; Conservative
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                                                                                       Similarity
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                                              Sequence 168 AA;
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Wood WI,
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                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; cardiant; vasotropic; antiarteriosclerotic; angiogenesis inhibitor; angiogenesis stimulator; angiogenic index; gene expression; cancer; coronary artery disease; myocardial ischemia; coronary arteriosclerosis; forensic medicine.
                                                                                                                                                                                                            389 EEDYEDDKDDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQER
                                                                                                                                    46 EEDYEDDKODDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQER
                                                                                                                                                                                    449 MIRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKV
                                                                                                                                                                                                                                                                             509 ISDLTPVSELPLTARPRSRKEKNKLAFRACRLKKKRAQYEANKVKLWGLNTEYDNLLFVIN
                                                                                                                                                                                                                                                                                                                                                                        SIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGG
                                                  Gaps
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                                                .
Length 296;
                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Angiogenesis-differentially expressed protein #50.
Score 150; DB 8;
Pred. No. 4e-137;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK65836 standard; protein; 91 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ischemia and/or arteriosclerosis.
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10-JUN-2002; 2002US-00164595.
16-AUG-2002; 2002US-0403649P.
03-JAN-2003; 2003US-0437746P.
    23.5%;
99.6%;
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    Query Match 23.5
Best Local Similarity 99.6
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVGLRIPTSKV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 LVGLRIPTSKV 296
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The invention relates to a method of determining the angiogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the angiogenic index. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary or oronary or or also be used in research, drug discovery and forensic medicine involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention. %%66666666688%%

Sequence 91 AA;

508 9 1 MLRPSEWNRDTLPSNWYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKV 449 MLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKV 0; Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 3.1e-72;
Matches 83; Conservative 0; Mismatches 0; Indels 509 ISDLTPVSELPLTARPRSRKEKN 531 Matches ઠે 유 8 원

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61 ISDLTPVSELPLTARPRSRKEKN 83

RESULT 7 ABG29275

ABG29275 standard; protein; 160 AA ABG29275; Novel human diagnostic protein #29266.

(first entry)

18-FEB-2002

Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.

WO200175067-A2.

11-OCT-2001

30-MAR-2001; 2001WO-US008631.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC.

Tang YT Drmanac RT, Liu C,

WPI; 2001-639362/73. N-PSDB; AAS93462.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 59634; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a

The present invention describes a method for detecting a stress that alters a functional interaction of a low density lipoprotein (LDL) (Teceptor binding protein (I) with an LDL receptor interaction domain (II). The method involves introducing a predetermined stress into a system which provides a stress-biased physical interaction of (I) with (II), where in the absence of the stress, the system provides an unbiased interaction of (I) and (II), and detecting the stress-biased interaction of (I) and (II), where a difference between BI and UI indicates that the stress alters the interaction of (I) and (II). (I) is selected from SEMCAP-1, JIP-1, PSD-95, JIP-2, Tallin, OMP25, CAPON, PIP4,5 Kinase, Na channel brain 3, Mintl, ICAP-1 and APC subunit 10. The method is useful for detecting a stress that alters functional interaction of LDL receptor

ö polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at Itp.wipo.int/pub/published_pct_sequences Low density lipoprotein receptor binding protein; signal transduction; LDL receptor signalling pathway. Detecting stress that alters interaction of LDL receptor binding polypeptide with LDL receptor interaction domain, comprises detecting difference in stress-biased and unbiased interaction of peptide and Gaрв ö Length 160; 0; Indels 601 29 NLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTL 68 562 NLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTL 6.3%; Score 40; DB 4; Lo 100.0%; Pred. No. 4.4e-30; ative 0; Mismatches 0; LDL receptor binding protein JIP-2 SEQ ID NO:35. Disclosure; Page 78-79; 200pp; English. ABB04812 standard; protein; 830 AA 24-APR-2001; 2001WO-US013214. 01-MAY-2000; 2000US-00562737. (first entry) (TEXA) UNIV TEXAS SYSTEM. Conservative Gotthardt M; WPI; 2002-082855/11. domain in a system. Local Similarity Sequence 160 AA; WO200184159-A2 08-NOV-2001. 13-MAR-2002 40; Synthetic ABB04812; Query Match Herz J, Best Loc Matches ABB04812 RESULT 8888888888888888888888888 ð 셤

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1000 SENEEEEEEE 1010
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Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH62819.
                                                                                                                                                                                                                                                                                                                                                                                        WO200138351-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-NOV-1999;
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11-SEP-2001
                                                                                                                                                                     AAG85039;
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ID ADF6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and concoded proteins (AAG84910-AAG85051) and oligomucleotide sequences (AAH62840-63160) suitable for use as primers or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral agene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides the primary nucleotide sequence of the WSBV genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic viral resistant shrimp. (Updated on 06-AUG-2003 to correct OS
binding polypeptide with LDL receptor interaction domain. The method is useful for detecting and modulating signal transduction through LDL receptors. ABB04778 to ABG04909 represent LDL receptor binding proteins which are used in the exemplification of the present invention
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                                                                                                                  1.7%; Score 11; DB 5; Length 830;
100.0%; Pred. No. 0.36;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiviral agent, gene expression; antisense construct; transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                                                                                                                                                       Shrimp white spot Bacilliform virus (WSBV) protein 21.
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(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
(SINO-) SINOGENOMAX CO LTD.
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                                                                                                                                                                                                                                                                                                       AAG84930 standard; protein; 1100 AA.
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                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White spot syndrome virus.
                                                                                                                                                  11; Conservative
                                                                                                                                                                                                           FNEEEEEEEE 104
                                                                                                                                                                                     381 ENEEEEEEED 391
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                                                                                                                                                                                                                                                                                                                                                                         (revised)
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                                                                                                                   Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                    Sequence 830 AA;
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11-SEP-2001
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AAG84930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primary nucleotide sequence of the shrimp white spot Bacilliform virus (WSBV), useful for producing viral polypeptides that can be used to screen for agents that are useful for treating WSBV infection.
                                                                                                                                                                                                                                                                                    Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; transgenic viral resistant shrimp.
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                                                                                                                                                                                                                             Shrimp white spot Bacilliform virus (WSBV) protein 130.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PENY-) PE CORP NY.
(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
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100.0%; Pred. No. 0.48;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADF69140 standard; protein; 1483 AA.
AAG85039 standard; protein; 1174 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 3; 626pp; English
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                                                                                                                                   (revised)
(first entry)
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12-FEB-2004

09-OCT-2003

Belvin M, Funke RP;

activity.

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which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic and sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for detecting soft tissue sarcoma
                                                                                                                                                                                                                                                                                                                                               Barly detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; cyclin-dependent kinase; cdk; biomarker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.7%; Score 11; DB 8;
100.0%; Pred. No. 0.59;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 3730; 210pp; English.
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                                                                                                                                                                                                                   (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-2004; 2004WO-US024424.
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                                                                                                                                                                       26-NOV-2002; 2002US-0429739P.
                                                                                                                            26-NOV-2003; 2003WO-US038193.
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                                                                                                                                                                                                                                                              Aziz N, Ginsburg WM,
                                                                                                                                                                                                                                                                                                          WPI; 2004-441208/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1483 AA;
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                                         WO2004048938-A2
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  Homo sapiens.
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                                                                                    10-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for identifying a candidate p53 pathway modulating agent, which comprises: (a) providing an assay system comprising a mp53 (modulator of p53) polypeptide or nucleic acid or its fragment or derivative; (b) contacting the assay system with a test agent conditions where the system provides a reference activity except in the presence of the test agent; and (c) detecting a test agent-biased activity, where a difference between the test agent as a candidate p53 pathway modulating agent; and secribed: (1) modulating the p53 pathway in a mammalian cell; and (3) diagnoshing a disease in a patient. MP53 has cytostatic activity, and can be used in gene therapy. The method is useful for identifying a candidate p53 pathway modulating agent for preparing a composition for diagnosing or treating e.g., cancer. The present sequence represents a human MP53 protein, which is useful the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a candidate p53 pathway modulating agent for treating e.g cancer by contacting an assay system comprising a MP53 polypeptide or nucleic acid with a test agent and detecting a test agent-blassed
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                                                                                                                                p53 pathway modulating agent; MP53; p53 modulator; cytostatic; gene therapy; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human soft tissue sarcoma-upregulated protein - SEQ ID 3730.
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100.0%; Pred. No. 0.59;
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                                                                                         Human MP53 protein sequence SEQ ID NO:110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Francis-Lang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                               (EXEL-) EXELIXIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-812540/76.
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Best Local Similarity
Matches 11; Conserv
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26-AUG-2004

ADQ20910;

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RESULT 12 ADQ20910

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Gaps

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0.59; 0.59; 0; Indels

Length 1483;

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This invention describes a novel method of predicting or determining whether a mammal will respond or is responding to an anti-cancer agent that medulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from 2774 biomarkers given in the specification (nuclectide sequence SEQ ID No:1246 (Genbark EST W38729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers. The cdk modulator is preferably N-5-[[5-(1,1-Dimethylethyl)-2-coxazolyl]methyllthio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-taratric acid salt. Note: The sequence data for this patent did not form the the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.init/pub/published pct sequences. This sequence represents a biomarker used in the method of the invention.
                                                                       Biomarkers useful for predicting or determining the response of a mammal to a cancer treatment comprising administration of a modulator of cyclin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomarkers useful for predicting or determining the response of a mammal to a cancer treatment comprising administration of a modulator of cyclindependent kinase activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 11; DB 9; Length 1483;
Pred. No. 0.59;
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                                                                                                                                                  Claim 5; SEQ ID NO 418; 141pp; English
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                                                                                                             dependent kinase activity.
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Best Local Similarity
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N-PSDB; ADX05854.
                 WPI; 2005-163068/17.
N-PSDB; ADX05852.
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This invention describes a novel method of predicting or determining whether a mammal will respond or is responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from 2774 biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers. The cdk modulator is preferably N-5-[[5-1,1-1]methylethyl].2-
oxazolylmethyllthiol-2-thiazolyl-4-piperidine carboxamide, 0.5-L-taratic acid salt. Note: The sequence data for this patent did not form tartaric acid salt. Note: The sequence data for this patent did not form directly from WIPO at ftp. wipo.int. publypublished pot sequences. This sequence represents a biomarker used in the method of the invention.
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BAZ2-beta; treatment; cancer; proliferative disorder; screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcriptional regulator gene family containing bromodomain - may be expressed in testis tissue and is useful for treatment of cancer and other proliferative disorders.
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100.0%; Pred. No. 0.59;
vative 0; Mismatches
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                 Claim 5; SEQ ID NO 420; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW81172 standard; protein; 1527 AA.
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Gaps

This sequence represents the human BAZ1-beta protein, a member of

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CC family of transcriptional regulator genes containing a bromodomain (BAZ, CC Bromodomain with Atypical Zinc finger) which are expressed specifically CC in testis tissue and also in certain tumour lines. Transgenic cells may CC be used for the preparation of the BAZ1-alpha, BAZ1-beta, BAZ2-alpha and CC BAZ2-beta proteins. These proteins can be used in the treatment of cancer cC and other proliferative disorders, and in screening of compounds for CC their binding ability to the expression products (e.g. for use as drugs CC by modulation of transcriptional regulation)

XX Sequence 1527 AA;
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 Query Match
 1.7%; Score 11; DB 2; Length 1527;

 Best Local Similarity 100.0%; Pred. No. 0.61;

 Matches 11; Conservative 0; Mismatches 0; Indels

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Gaps

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Search completed: February 28, 2006, 09:05:50 Job time : 188 secs This Page Blank (uspto)

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2: /cgn2_6/ptodata/1/iaa/f_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PcTuS COMB.pep:*
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TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
CURRENT APPLICATION WUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 75
LENGTH: 91
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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US-09-562-737-35
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APPLICANT: Herz, Joachim
APPLICANT: Getthardt, Michael
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 35
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Patent No. 6657054
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Patent No. 6428967
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ORGANISM: Artificial Seguence
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-164-595-75
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100.0%; Pred. No. 0.25;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.25;
tive 0; Mismatches 0; Indel8
                                                                                                                                       TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR ITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR STILE OF INVENTION: TRANSCRIPTIONAL REGULATOR PELLE REPERENCE: 06501-042001
CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REPERENCE: G0501-042002
CURRENT APPLICATION NUMBER: US/09/839,479
CURRENT FILING DATE: 2001-04-20
FRIOR FILING DATE: 1999-10-15
FRIOR FILING DATE: 1999-10-15
FRIOR FILING DATE: 1999-0-17
FRIOR FILING DATE: 1999-0-17
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FRIOR FILING DATE: 1997-10-24
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US-09-839-479-68
'Sequence 68, Application US/09839479
'Factent No. 6727222
US-09-418-710-69
Sequence 69, Application US/09418710
Patent No. 6596482
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 11, Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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; Sequence 7037, Application US/09949016; Patent No. 681239; GENERAL INFORMATION:
), APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 0.25;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.25;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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US-09-839-479-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1531
TYPE: PRT
CRGANISM: Homo sapiens
US-09-418-710-29
GENERAL INFORMATION:
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US-09-949-016-7037
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TYPE: PRT
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100.0%; Pred. No. 0.25;
tive 0; Mismatches 0; Indels
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Pred. No. 0.25;
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                                                                               Sequence 27, Application US/09418710

Patent No. 6596482

GENERAL INFORMATION:

APPLICANIV COMMATION:

TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR;

FILE REFERENCE: 06501-042001

CURRENT APPLICATION NUMBER: US/09/418,710

CURRENT FILING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: US/09/418,710

PRIOR APPLICATION NUMBER: US 9/310027

PRIOR FILING DATE: 1998-04-17

PRIOR PLILING DATE: 1997-04-18

PRIOR FILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 73

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 27

LENGTH: 1527
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TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/839,479
CURRENT APPLICATION NUMBER: US/09/839,479
CURRENT APPLICATION NUMBER: US/09/839,479
PRIOR APPLICATION NUMBER: US/09/418,710
PRIOR APPLICATION NUMBER: US/01/83
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: UP 9/310027
PRIOR APPLICATION NUMBER: UP 9/310027
PRIOR APPLICATION NUMBER: UP 9/310627
PRIOR APPLICATION NUMBER: UP 9/310637
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASELSEQ for Windows Version 4.0
LENGTH: 1527
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; Sequence 29, Application US/09418710
; Patent No. 6596482
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Patent No. 6727222
GENERAL INFORMATION:
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Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-09-418-710-27
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APPLICANT: Wallone, Marcy K.
APPLICANT: Wong, Brian R.
APPLICANT: Wong, Brian R.
APPLICANT: Powell, Mark
APPLICANT: Powell, Mark
TITLE OF INVENTION: Modulators of Leukocyte Activation, BIC Compositions and Methods of FILE REFERENCE: A-71314/RMS/DHR
CURRENT APPLICATION NUMBER: US/10/202,480
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                RESULT 13
US-09-270-767-57041
; Sequence 57041, Application US/09270767
; Patent No. 6703491
; General Information:
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REPRENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SIGO ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 57041
; LENGTH: 141
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100.0%; Pred. No. 0.41;
tive 0; Mismatches 0; Indels
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                            Length 141;
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                       1.6%; Score 10; DB 2;
100.0%; Pred. No. 0.26;
tive 0; Mismatches
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100.0%; Pred. No. 0.2
ative 0; Mismatches
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US-09-991-181-287
; Sequence 287, Application US/09991181
; Patent No. 6913919
; RENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10202480 Patent No. 6929923
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Best Local Similarity 100.
Matches 10; Conservative
                            Query Match 1.6
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                    536 RACRLKKKAQ 545
                                                                                                                                                               39 RACRLKKKAQ 48
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46 ENEEEEEEE
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US-10-202-480-4
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APPLICANT: Keath Weinstock et al
APPLICANT: Keath Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 23592
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Sequence 41799, Application US/09270767

Patent No. 6703431

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 41799

LENGTH: 141
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100.0%; Pred. No. 0.25;
tive 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-33
PRIOR FILING DATE: 2000-10-33
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER: OF SEQ ID NOS: 207012
SEQ ID NO 7037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-09-248-796A-23592
; Sequence 23592, Application US/09248796A
; Patent No. 6747137
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US-09-270-767-41799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23592
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Matches 11; Conservative
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; ORGANISM: Human
US-09-949-016-7037
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FILING DATE: 1998-06-05
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C53
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065181
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R FILING DATE: 1998-06-04

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R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088029

R APPLICATION NUMBER: 60/088030

R APPLICATION NUMBER: 60/088030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087609
R PILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087759
R FILING DATE: 1998-06-02
R FILING DATE: 1998-06-03
R FILING DATE: 1998-06-03
R APPLICATION NUMBER: 60/088021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/075945
R FILING DATE: 1998-02-25
R APPLICATION NUMBER: 60/078910
R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/083322
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R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
A PPLICATION NUMBER: 60/087106
R FILING DATE: 1998-05-28
R APPLICATION NUMBER: 60/087607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066770
                                                                                                                                                            Grimaldi, J.Christopher
                                                                                                                                                                                                                                                     Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                               Ferrara, Napoleone
Fong, Sherman
                                                                                                                                                                                                                                     Paoni, Nicholas F.
                                                                                                              Gerritsen, Mary E.
Goddard, Audrey
                                                                                              Gerber, Hanspeter
                                                                                                                                                                         Gurney, Austin L.
Kljavin, Ivar J.
                   Botstein, David
                                                                                                                                                                                                        Napier, Mary A.
                                                                                                                                             Godowski, Paul
      Baker, Kevin P
                                   Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                          Рап, Јашев
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R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088624
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088626
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08868
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090431
FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/088742
TLING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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LING DATE: 1998-06-17
PLICATION NUMBER: 60/089538
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ILING DATE: 1998-06-17
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
                                        FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-12
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FILING DATE: 1998-06-16
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ILING DATE: 1998-06-17
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Query Match
1.6%; Score 10; DB 2; Length 255; Best Local Similarity 100.0%; Pred. No. 0.44; Matches 10; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 1998-06-24
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PRIOR PILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090545
PRIOR PILING DATE: 1998-06-24
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δ g Search completed: February 28, 2006, 09:11:26 Job time : 48 secs

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61 SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATFALPFKETQELLL
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PRIOR APPLICATION NUMBER: US/10/164,595
PRIOR FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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19, Appl
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2e 3730, Ap
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Sequence 75, Appl
Sequence 59634, A
Sequence 35, Appl
                                                                       ; Search time 166 Seconds
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1608.391 Million cell updates/sec
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1 MPQPSVSGMDPPFGDAFRSH......TAEGNPTGGLVGLRIPTSKV 639
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-211-962-35
US-10-723-860-3730
US-09-839-479-68
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-09-989-723-287
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-09-989-727-287
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US-09-990-456-287
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US-10-702-148-68
US-09-839-479-27
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                                                                          February 28, 2006, 09:10:46
                                                                                                                                                                                                                                                                                                                                Post-processing: Listing first 45 summaries
                                                  OM protein - protein search, using sw model
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Match Length DB
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Length 639; Indels 9 9 120

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30	10	٠	255	m	US-09-989-293A-287			
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35	10	•	255	m	US-09-990-436-287			
36	10		255	m	US-09-993-687-287			
37	10		255	٣	US-09-989-734-287			
80	10		255	m	US-09-997-653-287			
68	10		255	m	US-09-989-724-287			
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, Publica	Publication No. US20050106579A1	o. us20(	3501065	794	Ţ.			
, GENERAI	GENERAL INFORMATION:	ATION:						
, APPLI(	ANT: O	rigene 7	rechnol	g	APPLICANT: OriGene Technologies, Inc	and Dollmontides		
TILLE .	REFERENCE	E: 111	negura 103 R1	ב ני	gorico	anninds/fros		
STEPPEN.	TT APPT.	NOTTACT	NIMBER		CITEDENT APPLICATION NIMBER: US/10/717.665			
. CIRRENT		FILING DATE:	2003-11-21	-1'	-21			

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US-10-450-763-59634
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                                                                                                                                                481 RRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVSELPLTARPRSRKEKNKLAFRACRL 540
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361 EEDVDDEDHDEGFGSEHELSENEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKEV 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 75, Application US/10717665
Publication No. US20050106579A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies, Inc
ATTLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
CURRENT FILING DATE: 2003-11-21
PRICR APPLICATION NUMBER: US/10/11,665
FRICR APPLICATION NUMBER: US/10/164,595
PRICR FILING DATE: 2002-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 59634, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICAMT: Hyseq.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT PFLICATION NUMBER: US/10/450,763
; CURRENT PFLICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR PLING DATE: 2001-03-30
; PRIOR PLING DATE: 2000-03-31
; PRIOR PLING DATE: 2000-03-31
; PRIOR PLING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: CUSTOM
: LEMCTH. 160
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100.0%; Pred. No. 9.4e-70;
tive 0; Mismatches 0;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 75
LENGTH: 91
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ORGANISM: Homo sapiens
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US-10-717-665-75
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Sequence 3730, Application US/10723860
; Sequence 3730, Application US/10723860
; Publication No. US20040253606A1
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Ginsburg, Nethods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION NUMBER: US/10/723,860
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patentin version 3.2
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Length 160;
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                                                                                                                               29 NLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILLIKDTL 68
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Herz, Joachim
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/10/211,962
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US/09/562,737
PRIOR APPLICATION NUMBER: US/09/562,737
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
                                                                                                   562 NLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTL
DB 5; Le
5.7e-29;
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100.0%; Pred. No. 0.55;
tive 0; Mismatches
Query Match 6.3%; Score 40; DB Best Local Similarity 100.0%; Pred. No. 5.7 Matches 40; Conservative 0; Mismatches
                                                                                                                                                                                                                                                    US-10-211-962-35
; Sequence 35, Application US/10211962
; Publication No. US20030082640A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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US-10-723-860-3730
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LENGTH: 830.
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SEQ ID NO 27
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100.0%; Pred. No. 0.94;
tive 0; Mismatches 0; Indels
                                                                                                          Sequence 68, Application US/09839479
Publication No. US2002003977941
GENERAL INFORMATION:
APPLICANT: JONES, MICHAEL H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REPRENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/839,479
CURRENT PILING DATE: 2001-04-20
FRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-10-24
FRIOR PELICATION NUMBER: US 9/310027
PRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-3/6-53-69

Publication No. US20030224405A1

GENERAL INPORMATION:
APPLICANT: JORGE, MICHAEL H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFRENCE: 0550-042001
CURRENT APPLICATION NUMBER: US/09/418,710

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-10-17

PRIOR FILING DATE: 1999-10-24

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 73

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 1525

TYPE: PRI
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
1266 EEEEEEEEDYE 1276
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US-10-376-537-69
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 68
LENGTH: 1525
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                                                                                                  US-09-839-479-68
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WS-10-702-148-68

US-10-702-148-68

Sequence 68, Application US/10702148

Publication No. US20040063145A1

GENERAL INFORMATION:

APPLICATION NO.

TILLE OF INVENTION: TRANSCRIPTIONAL REGULATOR

FILE REFERENCE: 66501-042002

CURRENT APPLICATION NUMBER: US/10/702,148

CURRENT PILING DATE: 2003-11-05

PRIOR FILING DATE: 2003-11-05

PRIOR FILING DATE: 1999-10-10

PRIOR FILING DATE: 1999-10-10

PRIOR PILING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: PCT/JP98/01783

PRIOR APPLICATION NUMBER: PCT/JP98/01783

PRIOR APPLICATION NUMBER: DP 9/310027

PRIOR FILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH 15-05
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100.0%; Pred. No. 0.94;
tive 0; Mismatches 0; Indel8
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TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REPERENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/813,479
CURRENT FILING DATE: 2001-04-20
FRIOR PELICATION NUMBER: US 09/418,710
FRIOR PELICATION NUMBER: BT 09/418,710
FRIOR PELICATION NUMBER: PCT/JP98/01783
FRIOR PILING DATE: 1999-04-15
FRIOR PILING DATE: 1999-04-14
FRIOR PILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
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Best Local Similarity 100.
Matches 11; Conservative
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Matches 11; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-479-27
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US-10-702-148-68
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US-09-839-479-27
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LENGTH: 1531
TYPE: PRT
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US-10-702-148-27
Sequence 27, Application US/10702148
Publication No. US20040063145A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/10/702,148
CURRENT FILING DATE: 2003-11-05
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/99/839,479
FRIOR FILING DATE: 1001-04-20
FRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-10-15
FRIOR FILING DATE: 1999-10-15
FRIOR FILING DATE: 1998-04-17
FRIOR FILING DATE: 1998-04-17
FRIOR APPLICATION NUMBER: US 9/310027
FRIOR APPLICATION NUMBER: US 9/310027
FRIOR APPLICATION NUMBER: US 9/310027
FRIOR APPLICATION NUMBER: US 9/310570
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FRIOR APPLICATION NUMBER: US 9/3105
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100.0%; Pred. No. 0.94;
iive 0; Mismatches 0; Indels
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                        Sequence 27, Application US/10376537
Publication No. US20030224405A1
GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 05501-04201
CURRENT APPLICATION NUMBER: US/09/418,710
FRIOR FILING DATE: 2003-02-28
FRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-0-15
PRIOR FILING DATE: 1999-04-17
PRIOR FILING DATE: 1997-04-17
PRIOR FILING DATE: 1997-04-17
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FASTESE for Windows Version 4.0
SEQ ID NO 27
LENGTH: 1527
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Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-10-376-537-27
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ORGANISM: Homo sapiens
US-10-702-148-27
-10-376-537-27
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Sequence 29, Application US/10376537

Publication No. US20030224405A1

GENERAL INFORMATION:

APPLICANT: Jones Michael H.

TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR

FILE REFERENCE: 06501-042001

CURRENT APPLICATION NUMBER: US/10/376,537

CURRENT FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-10-15

PRIOR PILING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: PCT/JP98/01783

PRIOR PILING DATE: 1999-10-24

PRIOR APPLICATION NUMBER: US/9/310027

PRIOR APPLICATION NUMBER: US/9/116570

PRIOR PILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 73

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 29
Sequence 29, Application US/09839479
Publication No. US20020039779A1
GENERAL INFORMATION:
APPLICANT: JONES, MICHAEL H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REPRENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/819,479
CURRENT FILING DATE: 2001-04-20
FRIOR FILING DATE: 1999-10-15
FRIOR FILING DATE: 1999-10-15
FRIOR FILING DATE: 1998-04-17
FRIOR FILING DATE: 1998-04-17
FRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
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1.7%; Score 11; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 11; Conservative 0; Mismatches 0
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US-10-702-148-29
Sequence 29, Application US/10702148
Publication No. US20040063145A1
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RESULT 15
US-10-425-115-204867

Sequence 204867, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Vongwei
APPLICANT: Zhou, Yihua
APPLICANT: APPLICANT: ANOUISIC Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Number: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 204867

LENGTH: 102

TYPE: PRT

CORMAISM: Zea mays
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GENERAL INFORMATION:

APPLICANT: JORGE, Michael H.

IITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR

FILE REPERBNCE: 06501-04202

CURRENT APPLICATION NUMBER: US/10/702,148

CURRENT APPLICATION NUMBER: US/09/839,479

PRIOR PILING DATE: 2001-04-20

PRIOR PILING DATE: 1909-10-15

PRIOR APPLICATION NUMBER: PCT/JP98/01783

PRIOR PILING DATE: 1999-10-15

PRIOR PILING DATE: 1999-04-17

PRIOR PILING DATE: 1999-04-17

PRIOR PILING DATE: 1999-04-17

PRIOR PILING DATE: 1999-04-17

PRIOR PILING DATE: 1999-04-17

PRIOR PILING DATE: 1999-04-17

PRIOR PILING DATE: 1997-04-18

PRIOR PILING DATE: 1997-04-18

PRIOR PILING DATE: 1997-04-18

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 29

LENGTH: 1531
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100.0%; Pred. No. 0.94;
tive 0; Mismatches 0; Indels
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US-10-425-115-204867
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
GRGANISM: Homo sapiens
US-10-702-148-29
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Search completed: February 28, 2006, 09:14:18 Job time : 167 secs

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ORGANISM: Homo sapiens
US-11-040-488-2
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LENGTH: 593
TYPE: PRT
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Sequence 90, Appl
Sequence 2850, Ap
Sequence 308, Appl
Sequence 16, Appl
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Sequence 74, Appl
Sequence 34, Appl
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500.682 Million cell updates/sec
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1 MPQPSVSGMDPPFGDAFRSH.....TARGNPTGGLVGLRIPTSKV
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1: /cgn2 6/ptodata/2/pubpāa/USOB NEW PUB.pep:*
2: /cgn2 6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2 6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
5: /cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
6: /cgn2 6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*
7: /cgn2 6/ptodata/2/pubpaa/USO1 NEW_PUB.pep:*
7: /cgn2 6/ptodata/2/pubpaa/USO1 NEW_PUB.pep:*
8: /cgn2 6/ptodata/2/pubpaa/USO1 NEW_PUB.pep:*
                            GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-11-098-686-10232
US-10-821-234-1345
US-10-821-234-1254
US-11-067-425A-71
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US-11-078-189-14
US-11-044-289-29
US-11-054-281-107
US-11-126-313-31
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US-10-821-234-1170
US-10-714-887-122
US-11-072-512-3096
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                                                                                                                                       OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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26 8 1.3 355 7 US-11.122-1573-39 Sequence 2, Appli 29 Appli 29 B 1.3 355 7 US-11.122-1573-39 Sequence 10.9 Appli 29 B 1.3 417 6 US-105-135-45 Sequence 10.9 Appli 29 B 1.3 417 6 US-105-135-45 Sequence 10.9 Appli 20 B 1.3 417 6 US-105-135-45 Sequence 10.4 Appli 20 B 1.3 427 6 US-105-135-45 Sequence 10.4 Appli 20 B 1.3 427 6 US-105-135-45 Sequence 10.4 Appli 20 B 1.3 427 6 US-105-135-45 Sequence 10.4 Appli 20 B 1.3 427 6 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 427 6 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 427 6 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 427 6 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 427 6 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 555 7 US-11-235-135-130 Sequence 10.4 Appli 20 B 1.3 555 7 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 555 7 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 555 7 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 555 7 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 565 7 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 565 7 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 565 7 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 565 7 US-105-135-135 Sequence 10.4 Appli 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence 20 B 1.3 565 7 US-105-135-135 Sequence
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Sequence 1170, Application US/10821234
; Sequence 1170, Application US/10821234
; Publication No. US20050255114A1
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT PILING DATE: 2004-04-07
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SEQ ID NO 1170
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APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NACHIKAWA, TSUTOMU
APPLICANT: NACHARWA, TSUTOMU
APPLICANT: NACHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT FILING DATE: 2005-03-07
PRIOR PILING DATE: 2005-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3158
LENGTHA 268
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1.4%; Score 9; DB 7
Best Local Similarity 100.0%; Pred. No. 0.4
Matches 9; Conservative 0; Mismatches
  Mismatches
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; Sequence 3158, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
  ;
                                                                                                                                                                                                                                                ISOGAL, TAKAO
SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUUKO
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  9; Conservative
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IRIE, RYOTARO
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Squence 74, Application US/11067425A

Squence 74, Application US/11067425A

Squence 74, Application No. US20050278803A1

GENERAL INFORMATION:
APPLICANT: Hannoufa, Abdelali
APPLICANT: Lydiate, Derek J.
APPLICANT: Gao, Ming-Jun

TITLE OF INVENTION REGULATION OF GENE EXPRESSION USING CHROMATIN REMODELLING FACTORS
TITLE OF INVENTION NUMBER: US/11/067,425A

CURRENT FILING DATE: 2005-02-22

PRIOR PPLICATION NUMBER: US 10/516,753

PRIOR PPLICATION NUMBER: PT/CA03/00822

PRIOR APPLICATION NUMBER: US 60/387,088

PRIOR APPLICATION NUMBER: US 60/387,088

PRIOR PPLING DATE: 2002-06-06

NUMBER OF SEQ ID NOS: 108

SOFTWARE: Patentin version 3.3

SEQ ID NO 74

LENGTH: 221
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; Sequence 34, Application US/11063343
; Publication No. US20050272061A1
; GENERAL INFORMATION:
; APPLICANT: Petroziello, Joseph M.
APPLICANT: Carter, Paul
TITLE OF INVENTION: Lung Cancer
; TITLE OF INVENTION: Lung Cancer
; FILE REFERENCE: 26811-003N
; CURRENT APPLICATION NUMBER: US/11/063,343
; CURRENT FILING DATE: 2004-02-22
; PRIOR FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
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Pred. No. 0.34;
                                                                                                      Query Match
1.4%; Score 9; DB 6
Best Local Similarity 100.0%; Pred. No. 0.3
Matches 9; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 0.3
Matches 9; Conservative 0; Mismatches
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  ; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1443
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ORGANISM: Homo sapiens
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US-11-067-425A-74
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Publication No. US20060015972A1

GENERAL INFORMATION;

APPLICANT: HEARD, Jacqueline

APPLICANT: HEARD, Jacqueline

APPLICANT: RIECHMAN, Jose Luis

APPLICANT: CANALES, Roger

APPLICANT: REPETAT, Peter

APPLICANT: REPETAT, Peter

APPLICANT: RUMIMOTO, Roderick W

APPLICANT: RUMIMOTO, Roderick W

APPLICANT: BENERT, Liynne

APPLICANT: BENERY T. Liynne

APPLICANT: BENERY T. Liynne

APPLICANT: BENERY T. Liynne

APPLICANT: BENERY T. Liynne

APPLICANT: PINEDA, Omalra

APPLICANT: PINEDA, Omalra

APPLICANT: PINEDA, Omalra

APPLICANT: PINEDA, Omalra

APPLICANT: PINEDA, Omalra

APPLICANT: PINEDA, Omalra

CURRENT PILIS PETER MB10058-CIP

CURRENT APPLICATION NUMBER: US/10/714,887

CURRENT FILING DATE: 2003-11-13
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PRIOR APPLICATION NUMBER: 10/412,699
PRIOR FILING DATE: 2003-11-13
PRIOR FILING DATE: 2003-04-10
PRIOR FILING DATE: 2003-04-10
PRIOR PILING DATE: 1999-00-2-17
PRIOR PILING DATE: 1999-00-2-17
PRIOR PILING DATE: 1999-00-32
PRIOR PILING DATE: 1999-00-33
PRIOR PILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR PILING DATE: 2000-03-22
PRIOR PILING DATE: 2000-03-22
PRIOR PILING DATE: 2000-03-22
PRIOR PILING DATE: 2000-03-22
PRIOR PILING DATE: 2000-03-22
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PRIOR PILING DATE: 2000-03-22
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 1999-03-23
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
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PRIOR PILING DATE: 2000-11-16
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US-10-714-887-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4%; Score 9; DB 6; Length 427; 100.0%; Pred. No. 0.65; tive 0; Mismatches 0; Indels
                                                                                                                                                                  Length 414;
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ORGANISM: Oryza sativa (japonica cultivar-group)
                                                                                                                                                           Query Match
1.4%; Score 9; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 9; Conservative 0; Mismatches
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Best Local Similarity 100.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                    383 EEEEEEEED 391
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1170
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Gaps
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1.4%; Score 9; DB 7; Length 547;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                APPLICANT: HOLO, YORU
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: TRIE, KYOTARO
APPLICANT: TRIE, KYOTARO
APPLICANT: SEKI, NAOHIKO
APPLICANT: SEKI, NAOHIKO
APPLICANT: SEKI, NAOHIKO
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NACAHARI, KENJI
APPLICANT: NACHARI, KENJI
APPLICANT: NACHARI, KENJI
APPLICANT: NACHARI, KENJI
APPLICANT: NASHO, YASUHIKO
TITLE OF INVENTION: NOVEL full length CDNA
FILE REFERENCE: 08435-0191
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PALENTIN VET. 2.1
SENGTH: 547
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| Publication No. US20060029945A1 |
| Publication No. US20060029945A1 |
| GENERAL INFORMATION: |
| APPLICANT: SCGAI, TAKAO |
| APPLICANT: SUGIYAMA, TOMOYASU |
| APPLICANT: STO, HIROYUKI |
| APPLICANT: SATO, HIROYUKI |
| APPLICANT: SATO, HIROYUKI |
| APPLICANT: SATO, HIROYUKI |
| APPLICANT: ISHII, SHIZUKO |
| APPLICANT: HIO, YURI |
| APPLICANT: HIO, YURI |
| APPLICANT: HIO, YURI |
| APPLICANT: HIO, YURI |
| APPLICANT: HIO, YURI |
| APPLICANT: HIO, YURI |
| APPLICANT: HIE, RYOTARO
Sequence 3096, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                     APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIXAMA, TOMOYASU
APPLICANT: OTSUIL, TETSUII
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEKI, NACHIKO
YOSHIKAWA, TSUTCWU
OTSUKA, MOTOVUKI
NAGAHARI, KENJI
MASUHO, YASUHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAMECHIKA, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 EEEEEEED 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-11-072-512-3096
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A STANK

383 EEEEEEED 391

12 EEEEEEED 20

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APPLICANT: Hirsch, Joel
TITLE OF INVENTION: VOLTAGE-DEPENDENT CALCIUM CHANNEL BETA SUBUNIT FUNCTIONAL CORE
FILE REFERENCE: P-6758-US
CURRENT APPLICATION NUMBER: US/11/126,313
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0
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-240CLP
CURRENT APPLICATION NUMBER: 60/261,014
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR PELING DATE: 2001-01-11
PRIOR PELING DATE: 2001-01-11
PRIOR PELING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-10
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
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PRIOR PILING DATE: 2001-01-11
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                                                                                                                                                                                                                                                                                                                 Length 1178;
                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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1.4%; Score 9; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches
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                                                                                                                                                                                                      LOCATION: (1)...(1178) at all Xaa position; OTHER INFORMATION: Xaa = any amino acid US-11-044-899-29
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 107, Application US/11054281 Publication No. US20060013813A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31, Application US/11126313; Publication No. US20050288489A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 EEEEEEED 391
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                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                        NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-11-054-281-107
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                                                    SEQ ID NO 29
LENGTH: 1178
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                                                                                                                                                               FEATURE:
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Publication No. US20050260516A1

GENERAL INFORMATION:

APPLICANT: Schwah, M.

APPLICANT: Schwah, M.

TITLE OF INVENTION: THEREON
FILE OF INVENTION NUMBER: US/11/044,899
CURRENT FILING DATE: 2005-01-26
PRIOR PILICATION NUMBER: 09/830,972
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-06
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100.0%; Pred. No. 1;
tive 0; Mismatches
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100.0%; Pred. No. 1.1;
tive 0; Mismatches
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Sequence 14, Application US/11078189

Sequence 14, Application US/11078189

Publication No. US20050277167A1

GENERAL INFORMATION:

APPLICANT: Bachinger, Hans Peter

APPLICANT: Vranka, Janice

TITLE OF INVENTION: PROLYL 3-HYDROXYLASES

FILE REFERENCE: 08062-020001

CURRENT APPLICATION NUMBER: US/11/078,189

CURRENT FILING DATE: 2005-03-11

PRIOR APPLICATION NUMBER: US 60/552,409

PRIOR FILING DATE: 2004-03-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14
                        FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
FRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
LENGTH: 706
     TITLE OF INVENTION: Novel full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 US-11-072-512-3843
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Publication No. US20060024696A1

GENERAL INFORMATION:

APPLICANT: Kapur, Vivek and Gebhart, Connie J.

TITLE OF INVENTION: WCLEIC ACID AND POLYPEPTIDE SEQUENCES

TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING

FILE REFERENCE: 09531-12800.1

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: PCT/US03/31318

PRIOR APPLICATION NUMBER: US 60/416,395

PRIOR PILING DATE: 2003-10-04

NUMBER OF SEQ ID NOS: 11433

SOFTWARE: FASTERE OF EQ IN Windows Version 4.0

SEQ ID NO 10232

LENGTHER 8746
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US-11-044-111-24

Squence 24, Application US/11044111

Publication No. US20050272362A1

Publication No. US20050272362A1

GENERAL INFORMATION:

APPLICANT: Chiang, Wen

APPLICANT: Linz, John

TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys

TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys

CURRENT APPLICATION UNBER: US/11/044,111

CURRENT APLICATION UNBER: US/11/044,111

SOFTWARE: PATENTING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTIN VERSION 3.3

SEQ ID NO 24

LENGTH: 4868

TYPE: PRT

ORGANISM: Meleagris gallopavo

US-11-044-111-24
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1.4%; Score 9; DB 7; Length 8746;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels
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1.4%; Score 9; DB 7; Length 4868;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels
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1.4%; Score 9; DB 7; Length 2161;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2005-05-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31
LENGTH: 2161
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                                                                                                                       TYPE: PRT
ORGANISM: homo sapiens
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639
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## ALIGNMENTS

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A;Cross-references: UNIPARC:UP1000007CD27; EMBL:283239; PIDN:CAB05811.1; GSPDB:GN00023; (A;Experimental source: clone T09F5
                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-517 <WIL>
A;Residues: USI7 <WIL>
A;Cross-references: UNIPROT:017941; UNIPARC:UPI00007CD27; EMBL:Z81099; PIDN:CAB03189.1;
A;Experimental source: clone K08F9
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                                               hypothetical protein KO8F9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23499; T24766
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A;Introns: 16/2; 44/2; 66/2; 277/2; 341/3; 410/2; 426/3
C;Superfamily: Caenorhabditis elegans hypothetical protein K08F9.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                R.Mortimore, B.
submitted to the EMBL Data Library, December 1996
A;Reference number: 219933
A;Accession: T24766
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Ablecule type: DNA
A;Residues: 1-517 <WI2>
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submitted to the EMBL Data Library, October 1996
A,Reference number: Z19748
A,Accession: T23499
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RESULT T17401

Library transcription regulator WBSCR9 - mouse
N.Alternate names: Williams-Beuren syndrome deletion transcript 9 homolog
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Accession: T1401
R,Peoples, R.J.; Cisco, M.J.; Kaplan, P.; Francke, U.
Cytogenet. Cell Genet. 82, 238-246, 1998
A,Fittle: Identification of the WBSCR9 gene, encoding a novel transcriptional regulator, i
A,Reference number: Z18735; MUID:99077764; PMID:9858827
A,Accession: T17401
A,Status: preliminary; translated from GB/EMBL/DDBJ

Tue Feb 28 11:30:09 2006

C, Genetica:

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Nicontains: progesterone receptor form A C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 18-Nov-1994 #sequence revision 18-Nov-1994 #text change 09-Jul-2004
C; Accession: A35466; S06284; A40903; A24661; A24312; A40911; A61552
R; Jeltesh, J.M.; Turcotte, B.; Garnier, J.M.; Lerouge, T.; Krozowski, Z.; Gronemeyer, H.; J. Biol. Chem. 265, 3867-374, 1990
A; Title: Characterization of multiple mRNAs originating from the chicken progesterone rec A; Reference number: A35466; MUID:90154085; PMID:2303488
A; Recession: A35466
A; Status: translation not shown
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A; Title: Sequence and expression of a functional chicken progesterone receptor.
A; Reference number: A40903; MUID:91042592; PMID:3153474
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A; Residues: 1-786 <UEL>
A; Residues: 1-786 <UEL>
A; Cross-references: UNIPROT:P07812; UNIPARC:UP100001321A4; GB:M32732; GB:J05240; NID:921;
A; Cross-references: UNIPROT:P07812; UNIPARC:UP100001321A4; GB:M32732; GB:J05240; NID:921;
A; Gronsemeyer, H.; Turcotte, B.; Quirin-Stricker, C.; Bocquel, M.T.; Meyer, M.E.; Krozows)
EMBO J. 6, 3985-3994, 1987
A; Title: The Ohicken progesterone receptor: sequence, expression and functional analysis.
A; Reference number: S06284; MUID:88166640; PMID:3443098
A; Accession: S06284
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A;Residues: 128-133, E',135-147, E', 149-164 <CO2>
A;Cross-references: UNIPARC:UPI0000177C0A
A;Note: the authors translated the codon CAG for residue 7 as Glu and CAG for residue 21
A;Note: the authors translated the codon CAG for residue 7 as Glu and CAG for residue 21
R;Jeltsch, J.M.; Krozowski, Z.; Quirin-Stricker, C.; Gronemeyer, H.; Simpson, R.J.; Garni
Proc. Natl. Acad. Sci. U.S.A. 83, 5424-5428, 1986
A;Title: Cloning of the chicken progesterone receptor.
                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-571 a POH3-
A;Cross-references: UNIRROT: B36076; UNIPARC:UPI0000052F06; EMBL:228088; NID:9486130; PID:
A;Experimental source: strain S288C
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
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                                                           nypothetical protein YKL088w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                 CJACCESSION: 377913 #UE
CJACCESSION: 377913
R;Pohl, T.M.; Pohl, F.M.
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37897
A;Accession: S37913
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A;Map position: 11L
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A; Residues: 1-786 <GRO>
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NyAlternate names: protein F13112.40
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Species 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45635
S;Accession: T45635
S;Achoisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa submitted to the Protein Sequence Database, November 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q57530; UNIPARC:UP100000BEEC9; EMBL:X74123; NID:9510732; PID A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1993 C;Superfamily: T-6b protein
                          A;Residues: 1-1479 <PEO>
A;Cross-references: UNIPROT:Q9Z277; UNIPARC:UPI0000029780; EMBL:AF084480; NID:g4165088;
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A.Title: Oncogene arrangement in a shooty strain of Agrobacterium tumefaciens. As Reference number: 846509; MUID:94272016; PMID:8003699
A.Accession: 846510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 26-Dec-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
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A;Experimental source: cultivar Columbia; BAC clone F13112
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tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.19;
ive 0; Mismatches 0; Indels
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A;Map position: 5
F;1360-1415/Domain: bromodomain homology <BRO>
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Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              383 EEEEEEEDYE 393
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-547 <CHO>
A; Molecule type: mRNA
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A;Map position: 3
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C, Genetics:

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T45635

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A;Residues: 1-1361 <ODE>
A;Cross-references: UNIPROT:Q04693; UNIPARC:UPI00000530F0; EMBL:Z47816; NID:g642303; PIDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wypothetical protein YML049c - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein YM9827.03c
C;Species: Saccharomyces cerevisiae
C;Date: 10.Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Date: 10.Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accesion: S5043
S;Odell, C.; Bowman, S.
submitted to the EMBL Data Library, January 1995
A;Reference number: S50941
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
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                                                                                                                                A;Map position: 16L
C;Superfamily: yeast NAB3 protein; ribonucleoprotein repeat homology
C;Keywords: nucleus; RNA binding
F;331-396/Domain: ribonucleoprotein repeat homology <RRM1>
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100.0%; Pred. No. 0.43;
tive 0; Mismatches
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100.0%; Pred. No. 0.35;
tive 0; Mismatches
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1.6%; Score 10; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 10; Conservative 0; Mismatches
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A,Map position: 13L
                                           C;Genetics:
A;Gene: SGD:NAB3; NAB3; HMD1; MIPS:YPL190c
A;Cross-references: SGD:S0006111
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Matches 9; Conservative
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nes 10; Conserv
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A; Status: preliminary
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A;Introns: 5/1
A;Note: F17C15.130
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N.Alternate names: probable RNA/ssDNA-binding protein HMD1; protein P1945; protein YPL19

N.Alternate names: probable RNA/ssDNA-binding protein HMD1; protein P1945; protein YPL19

C.Species Saccharomyces cerevisiae

C.Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004

C.Accession: S48529; S65209; S60122

C.Accession: S48529; S65209; S60122

R.Wilson, S.M.; Oberdorf, A.M.; Datar, K.V.; Swedlow, J.R.; Paddy, M.R.; Swanson, M.S.

Submitted to the EMBL Data Library, January 1994

A.Description: Characterization of Nuclear Polyadenylated RNA-Binding Proteins from Saccharomer.
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A;Residues: 1-802 <MIL>
A;Residues: 1-802 <MIL>
A;Crose-references: UNIPROT:P38996; UNIPARC:UPI000004F979; EMBL:U05314; NID:g476219; PID
R;Rieger, M.; Mueller-Auer, S.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S65202
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      A;Molecule type: protein
A;Residues: 136-153;168-174;195-228;526-537,'X',539;546-563 <SIM>
A;Cross-references: UNIPARC:UP10000177C0C; UNIPARC:UP10000177C0D; UNIPARC:UP10000177C0E;
C;Genetics:
                                                                                                                                                                                                                     Mol. Endocrinol. 1, 249-259, 1987
A;Title: Chemical and antigenic properties of pure 108,000 molecular weight chick proges
A;Reference number: A40911; MUID:88288199; PMID:3453892
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A; Residues: 1-802 <RIE>
A; Residues: 1-802 <RIE>
A; Residues: 1-802 <RIE>
A; Residues: 1-802 <RIE>
A; Cross-references: UNIPARC: UP1000004F979; EMBL: Z73546; NID: g1370396; PID: g1370397; GSP
A; Experimental source: strain S288C (AB972)
R; Sugimoto, K.; Matsumoto, K.; Kornberg, R.D.; Reed, S.I.; Wittenberg, C.
Mol. Gen. Genet. 248, 712-718, 1995
A; Title: Dosage suppressors of the dominant G1 cyclin mutant CLN3-2: identification of A; Reference number: $60122; MUID: 96069710; PMID: 7476874
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 128-133, E',135-147, E',149-164;546-558 <BIR>
A;Residues: 128-133, E',135-147, E',149-164;546-558 <BIR>
A;Cross-references: UNIPARC:UPI0000177C0A; UNIPARC:UPI0000177C0B
R;Simpson, R.J.; Grego, B.; Govindan, M.V.; Gronemeyer, H.
Mol. Cell. Endocrinol. 52, 177-184, 1987
A;Title: Peptide sequencing of the chick oviduct progesterone receptor form B.
A;Reference number: A61552; MUID:88005426; PMID:3653503
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100.0%; Pred. No. 0.26;
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A; Residues: 1-340,'I',342-802 <SUG>
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Best Local S
Matches 10
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A;Molecule type: DNA
A;Residues: 1-184 <STO>
A;Cross-references: UNIPROT:022801; UNIPARC:UPI00000A10DC; GB:AE002093; NID:92459433; PII
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A;Residues: 1-190 <BUR>.
A;rossi-terences: UNIPROT:P05221; UNIPARC:UPI0000171574; GB:Y00204; NID:g64938; PIDN:C?
C;Superfamily: nucleophosmin
C;Keywords: molecular chaperone; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-166 cALES
A;Cross-references: UNIPROT:P26583; UNIPARC:UPI000016AA6C; EMBL:Z17240; NID:g32334; PIDN: A;Cross-references: UNIPROT:P26583; UNIPARC:UPI000016AA6C; EMBL:Z17240; NID:g32334; PIDN: A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992 C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology (c;Reywords: chromosomal protein F;1-60/Domain: HMG box homology (fragment) <HMG>
F;69-143/Domain: HMG box homology <HMG1>
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R;Burglin, T.R.; Mattaj, I.W.; Newmeyer, D.D.; Zeller, R.; De Robertis, E.M.
Genes Dev. 1, 97-107, 1987
A;Title: Cloning of nucleoplasmin from Xenopus laevis oocytes and analysis of its
A;Reference number: A26630; MUID:88112783; PMID:3428591
A;Accession: A26630
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nonhistone chromosomal protein HMG-2B - human (fragment)
C,Species: Homo sapiens (man)
C,Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
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R, Alexandre, S., Ili, W.W.; Lee, A.S.
Nucleic Acids Res. 20, 6413, 192 novel 3'-untranslated region.
A, Title: A human HMG2 cDNA with a novel 3'-untranslated region.
A, Reference number: S30221, MUID:93117123; PMID:1475204
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tive 0; Mismatches
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1.4%; Score 9; DB 2
Best Local Similarity 100.0%; Pred. No. 0.7
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A;Status: preliminary
                                                                                                                                                 A; Map position: 2
                                                                                                                    C;Genetics:
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A;Experimental source: strain Bristol N2; clone C16H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fine. K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987

Nucleic Acids Res. 15, 5051-5068, 1987

Aritie: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA A; Reference number: A27853; MUID:87259986; PMID:3601666

A; Rocession: A27853

A; Molecule type: mRNA
A; Residues: 1-170 <LEE>
A; Cross-references: UNIPROT:P07156; UNIPARC:UP100001771D5
C; Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C; Superfamily: nonhistone chromosomal protein; DNA binding; nucleus
F;1-38/Domain: HMG box homology (fragment) <HMG1>
F;47-121/Domain: HMG box homology <HMG2>
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                                                                                                           hypothetical protein C16H3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T30045
R;Geisel, C.; Bradshaw, H.
Bubmitted to the RMBL Data Library, August 1996
A;Description: The sequence of C. elegans cosmid C16H3.
A;Accession: T30045
A;Accession: T30045
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: L136 <GEI>
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C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A27853
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100.0%; Pred. No. 0.69;
tive 0; Mismatches 0; Indels
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Local Similarity 100. nes 9; Conservative

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A; Gene: CESP: C16H3.4 A; Map position: X A; Introns: 26/1

C;Genetics:

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hypothetical protein At2g33510 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: D84746
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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Query Match

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RESULT 12 D84746

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RESULT 15
A26169
Uncleoplasmin - African clawed frog
C; Cipecies: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C; Accession: A26169
R; Dingwall, C:; Dilworth, S.M.; Black, S.J.; Kearsey, S.E.; Cox, L.S.; Laskey, R.A.
EMBO J. 6, 69-74, 1987
A; Title: Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and a cluster of shapefacene number: A26169; MUID:87218476; PMID:2884102
A; Accession: A26169
A; Molecule type: mRNA
A; Residues: 1-200 cDIN>
A; Accession: A26169
A; Molecule type: mRNA
A; Residues: 1-200 cDIN>
C; Superfamily: nucleophosmin
C; Keywords: molecular chaperone; nucleus
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1.4%; Score 9; DB 2; Length 200;
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Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A popular R.F., Jordan H., Moore T., Mang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schain J.B., Jones S.J.M., Marra M.A.;
R. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                           QBIURG, HUMAN PRELIMINARY; PRT; 639 AA.
QBIURG;
QBIURG;
O1-MAR-2003 (TYEMBLrel. 23, Created)
O1-MAR-2003 (TYEMBLrel. 26, Last annotation update)
O1-MAR-2004 (TYEMBLrel. 26, Last annotation update)
Adult retina protein.
Name=LOC15222;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                         421 TSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKS
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                                                                         RRIDVEDLIPNPKKLLQIGNELRKLNKVISDLIPVSELPLTARPRSRKEKNKLA
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0
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Director MGC Project;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041709; AAH41709.1; -; mRNA.
Ensembl; ENSG0000164463; Homo sapiens.
InterPro; IPR004827; TF bZIP.
PROSITE; PS000056; BZIP BASIC; UNRNOWN 1.
SEQUENCE 639 AA; 72I18 WW; ECFB92D9290DEDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.6%; Score 381; DB 2;
99.8%; Pred. No. 0;
iive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences.
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Matches 481, Conservative
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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AAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV
                               301 SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEED
                                                                                                                                                                                                                                                                                                                                                     361 EEDVDDEDHDEGFGSEHELSENEEEEEEEDVEDDKDDISDTFSEPGYENDSVEDLKEV
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                                                                                                     KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL
                                                                                                                                                                                                                                                                                                                         EEDVDDEDHDEGFGSEHELSENEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKEV
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EMBL, BX647768; CAI46039.1; -; mRNA.

Hypothetical protein.

NON TER

A08

A08

A18

SEQÜENCE

A08

A34

A5625 MW; E3E36BFEA8B4284B CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypotheital protein DKFZp686G2059 (Fragment).
Name=DKFZp686G2059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.0%; Score 307; DB 2; L 99.8%; Pred. No. 1.1e-292; tive 0; Mismatches 1;
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δ 셤 ò 셤

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241 KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQCHATPALPFKETQELLL 300
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                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinee; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930001N09 product:hypothetical protein, full insert sequence
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TISSUB=Adipose;
The German cDNA Consortium;
The German cDNA Consortium;
Kochrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX647573; CAIGL04.1; -; mRNA.
InterPro; IPR004827; TF_bZIP.
INTERPRO; IPR004827; TF_bZIP.
Hypothetical protein.
Hypothetical protein.
NON TER 604
                                                                                                                                                                                                                                                                                                                                          604 AA; 68572 MW; 977C229B63E2E4C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         42.6%; Score 272; DB 2; 1
99.6%; Pred. No. 4.2e-258;
tive 0; Mismatches 2;
Hypothetical protein DKFZp313F2319 (Fragment)
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Q9CTQ7;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 472; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                     Name=DKFZp313F2319
                                                                                                       NCBI_TaxID=9606;
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                                                          360
                     300
                                                                                           301 SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEED 360
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL
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1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX174896; AAO18732.1; -; mRNA.
Hypothetical protein.
SEQUENCE 417 AA; 46579 MM; 9DBD37B07C14556B CRC64;
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Last annotation update)
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8est Local Similarity 99.8%; Pred. No. 1.1e-292;
Matches 407; Conservative 0; Mismatches 1;
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QSHYKO;
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                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
Homo sapiens (Human).
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A KTARAIO-CSTEL/GOI, TISSUE-Retina;
A RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Radota K., Matsuda H.A., Gissi C., King B., Kochiwa H.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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MEDIJNE=20499374; PUMPd=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes.";

Genome Res. 10:1617-1630 (2000).
                                                                    STRAIN=C57BL/60; TISSUE=Retina;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length_cDNA cloning.";
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                                                                                                                                                                               Enzymol. 303:19-44(1999)
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NCBI_TaxID=10090;
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Rawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S., A Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Shisohman W., Gasterland T., Gissi C., King B., Kochiwa H., Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bronstein M.J., Bult C., Fluther C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S., Hayashizaki Y.
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Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930040G19 product:hypothetical protein, full insert sequence.
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                 330 AA; 36692 MW; 1397555C4934A64B CRC64;
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Pred. No. 2.8e-76;
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Basembl; RNSWMSG00000048249; Mus musculus.
MGI; MGI:1924778; A930001N09Rik.
Hypothetical protein.
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clone:4932441F15 product:hypothetical protein, full insert
                  sequence.
Name=A930001N09Rik;
Mus musculus (Mouse)
                                                                                                    NCBI_TaxID=10090;
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    library,
    C STRAIN-CSTAL/6J; TISSUB-Retina;
A Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Kilmotani K., Ishii Y., Itoh M., Kagawa T.,
A Hori F., Imotani K., Ishii Y., Kondo S., Konno H., Kouda M., Koya S.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Miyazaki R., Ohno M., Ohasto N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Asaaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Angawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Andaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

R MBL; AKO44760; BAC32070:1; -; mRNA.
R MBL; MC194378; A93000100048249; Mus musculus.
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                               STRAIN=C57BL/63; TISSUE=Retina; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nurmalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                             MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Ttoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Ttoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishinc H., Itoh M., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Poneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated asquence analysis (RISA) system-384-format geneuncing pipeline with 384 multicapillary sequencer.";
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01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
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01-MAR.2004 (TEMBLE1. 26,
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Matches 87; Conservative
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C STRAINE-CSTEL/G1 TISSIE-TESTIS;

NEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;

NA Arakawa T., Haniah Y., Kohno H., Rondo S., Yamanaka I.,

NA Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Na Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Na Chrimil L., Masteda H.A., Ashburner M., Batalov S., Casavant T.,

Nordone P., Nardion M., Suzuki R., Nikaido I., Pesole G., Quackenbush J.,

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Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Bronnetein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sakai H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Norman M., Wandel K.H., Weitz C., Whittaker C., Wilming L.,

Norman M., Wandel K.H., Weitz C., Whittaker C., Wilming L.,

Norman M., Wandel K.H., Weitz C., Whittaker C., Wilming L.,

Norman M., Wandel K.H., Weitz C., Whittaker C., Wilming L.,

Norman M., Wandel K.H., Weitz C., Whittaker C., Wilming L.,

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STRAIN-C57BL/6J; IISSUE=Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukarmalia; Butheria; Buarchontoglires; Glíres; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Testis;
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Nature 420:563-573(2002).
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayateno M., Haramoto K., Hisokar T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh K., Sakai K., Sakazume N., Sakai K., Sakai M., Sakai C., Sakai K., Sakai K., Sakai K., Sakai M., Sakai T., Sogabe Y., Tagami M., Togamu A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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100.0%; Pred. No. 2.5e-34;
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Last sequence update)
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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Q4RRX3;
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QSZMDS;
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Gallus gallus (Chicken).
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ORFNames=RCJMB04_2h14
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Mary J.M., Brunet F., Detit J.L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicad S., Jaffe D., Fisher S., Luffalla G., Dossat C., Sequrens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier D., Poulain J., De Berardinis V., Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., McEwan P., Bosak S., Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
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Rajendran K.V., Mukherjee S.C., Vijayan K.K., Jung S.J., Kim Y.J.,
Oh M.J.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY374443; AAQ92041.1; -; Genomic_DNA.
                                                                                                                                                                                         Tetraodon nigroviridis (Green puffer).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope, Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the BMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            600 AA; 66291 MW; B2F28B2F3B27B1C4 CRC64;
                        13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 7 SCAF15001, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18918 MW; BFCB713D3B1D081A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Wsv285 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.3%; Score 34; DB 2; Le
100.0%; Pred. No. 6.6e-24;
rative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501 ELRKLNKVISDLTPVSELPLTARPRSRKEKNKLA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAE01015001; CAG08859.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.7%; Score 11; DB 2;
100.0%; Pred. No. 0.093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 ELRKLINKVISDLTPVSELPLTARPRSRKEKNKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the early vertebrate proto-karyotype.";
31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MSSA)
                                                                                                                                                                    ORFNames=GSTENG00029962001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White spot syndrome virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGUAY4_WSSV PRELIMINARY;
QGUAY4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=92652;
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN-ATCC 36239 / CBS 767;

EDMAG=15229592; DOI=10.1038/nature02579;

EDMAG=15229592; DOI=10.1038/nature0279;

EDMAG=15229592; DOI=10.1038/nature0279;

EDMAG=10.1038/nature0279;

EDMAG=10.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology.";
EMBL; 283239; CABO3189.1; -; Genomic_DNA.
EMBL; Z83099; CABO3189.1; -; Genomic_DNA.
EMBL; Z83099; CABO5811.1; -; Genomic_DNA.
EMBL; Z83239; CABO5811.1; JOINED; Genomic_DNA.
EMBL; Z83239; T23499; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mortimore B.J.; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 AA; 53829 MW; FIC367DFC5FE8117 CRC64;
                                     Saccharomycetales; Saccharomycetaceae; Debaryomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 08, Last sequence update)
11-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein K08F9.4.
ORFNames=K08F9.4;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.7%; Score 11; DB 2;
100.0%; Pred. No. 0.23;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, CR382138; CAG89724.1; -; Genomic_DNA.
InterPro; IPR000313; PWWP.
Pfam; PF00855; PWWP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00293; PWWP; 1.
PROSITE; PS50812; PWWP; 1.
Complete proteome.
SEQUENCE 468 AA; 53829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CAEEL
OT7941 CAEEL PRELIMINARY;
O17941; 018079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 REFERENCE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 EEEEEEEDYE 200
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                                                             NCBI TaxID=4959;
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      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QJBS6 WSSV PRELIMINARY; PRT; 358 AA.

Q91BS6;

Q01BSC-2001 (TrEMBLrel. 19, Created)

01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Hypothetical protein.

White spot syndrome virus (WSSV).

Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
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Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.7%; Score 11; DB 2; Length 215;
100.0%; Pred. No. 0.12;
trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
Shi Z., Bonami J.-R.;
Submitted (JAN-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AF345568; AAL24459.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 358 AA; 40861 MW; FFF05A8AR12B2680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xia C., Liu J.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB021155; BAA83091.1; -; Genomic_DNA.
SEQUENCE 215 AA; 24441 MW; 913D2D116BBB7B5B CRC64;
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QGBKF1 DEBHA
AC GEBKF1.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DF 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DF 35-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unidentified baculovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
VCDI_TAXID=10469;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                       215 AA.
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Best Local Similarity 100.0%; Pred. No. U.1
Matches 11; Conservative 0; Mismatches
          Mismatches
                                                                                                                                                                                                                                                                                                       PRT;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
HHNBV-XIA.
                                                                                                                                                                                                                                                                                                QOOTF1 9BACU PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 SENEEEEEEE 268
                                                                                                                    92 SENEEEEEEE 102
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      11; Conservative
                                                                        380 SENEREEEEE 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=HHNBV-XIA;
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          Matches
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091B56

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Gaps

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Length 468; 0; Indels

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WormPep; K08F9.4; CE11948.
Complete proteome; Hypothetical protein.
SEQUENCE 517 AA; 59610 MW; 68E9E8909D5808FD CRC64;
     S W S
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; 0; Gaps Ouery Match 1.7%; Score 11; DB 2; Length 517; Best Local Similarity 100.0%; Pred. No. 0.25; Matches 11; Conservative 0; Mismatches 0; Indels

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Search completed: February 28, 2006, 09:09:46 Job time : 233 secs

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; Search time 153.45 Seconds (without alignments) 1282.772 Million cell updates/sec
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1 MPQPSVSGMDPPFGDAFRSH......GKRRYFWEYSEQLTPSQQER 448
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                        US-10-717-665A-44_COPY_1_448
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             February 28, 2006, 08:37:25
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2003bs:*
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Maximum DB seq length: 2000000000
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1: geneseq
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Angio	Novel	Novel	Human			_				Kapo	Rat	Rat	Rat	Rat	Aab85725 Rat TBP-b	Huma	Rat	Ade56302 Rat Prote	Adp46649 Human col	Human	Ade61625 Human Pro	Add46092 Human Pro	Aar79912 Human nuc
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SUMMARIES		ADK65805	ADQ66472	ADK35935	ABP64928	ADO20373	AAY96255	AAY58500	AAB62331	ABB05621	ADJ65096	ADV68154	ADE61623	ADD46090	ADE57828	ADE57830	AAB85725	AAE37016	AAW30749	ADE56302	ADP46649	ADP46648	ADE61625	ADD46092	AAR79912
	Ð	AD.	ă	Ş	ABI	ă	Ž	Ā	A	ABI	á	Ā	P	ADI	8	8	¥	¥	A	Ā	AD	8	Ā	Ā	¥
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	Length	639	417	256	168	296	1162	1162	1162	1162	1162	1162	712	712	712	712	842	735	712	712	520	568	706	706	707
	% Query Match	100.0	6.06	53.6	36.6	23.6	8.0	8.0	8.0	8.0	8.0	8.0	7.8	7.8	7.8	7.8	7.6	7.2	7.1	7.1	7.0	7.0	7.0	7.0	7.0
	Score	2364	2148	1268	865	557	190	190	190	190	190	190	185.5	185.5	185.5	185.5	179	169.5	168	168	165	165	165	165	165
	Result No.	-	7	m	4	ι.	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

The invention relates to a method of determining the angiogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the angiogenic index. The methods and compositions of the present

Claim 23; SEQ ID NO 44; 296pp; English.

		Adp25445 Plasmodiu Abg11270 Novel hum Aay58002 Saccharom		Abr64241 Angiogene Adp54420 Human PRO Aeb22180 Codon opt Aeb22174 Plasmodiu Abb70151 Drosophil
AAW84052 AAB48964 ADD49220 ADJ58974	ADP54086 ADY19864 ABM80398 ADZ72253	ADP25445 ABG11270 AAY58002	ADC08999 ABG04351 ADN22802 AAE18907 AAW81171	ABR64241 ADP54420 AEB22180 AEB22174 ABB70151
07 2 07 4 07 7 07 8	707 8 707 9 710 8 354 9	71 8 67 4 31 3	0 4 8 2 7 7 7 2 5 8 2 8 2 2 2 5 8 8 2 2 2 5 8 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	1972 6 1972 8 3147 9 3553 9
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## ALIGNMENTS

cytostatic; cardiant; vasotropic; antiarteriosclerotic; angiogenesis inhibitor; angiogenesis stimulator; angiogenesis stimulator; angiogenesis gene expression; cancer; coronary artery disease; myocardial ischemia; coronary arteriosclerosis; forensic medicine. Determining the angiogenic index of a tissue or cell sample using expression levels of differentially expressed genes, useful for diagnosing or treating cancer, coronary artery disease, myocardial ischemia and/or arteriosclerosis. Anglogenesis-differentially expressed protein ANH0757. Jay G; ADK65805 standard; protein; 639 AA. Li X, Kovacs KF, Fan W, (ORIG-) ORIGENE TECHNOLOGIES INC. 07-FEB-2002; 2002US-00067482. 10-JUN-2002; 2002US-00164595. 16-AUG-2002; 2002US-0403649P. 03-JAN-2003; 2003US-0437746P. 07-FEB-2003; 2003WO-US003848 (first entry) WPI; 2003-731502/69. N-PSDB; ADK65804. WO2003066831-A2. Homo sapiens 06-MAY-2004 14-AUG-2003. ADK65805; Sun Z, ADK65805  ŝ Ishii

ij Sato

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
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 treating cancer,
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                                                                                                                                         Gaps
invention are useful for diagnosing, preventing and/or treating canc coronary artery disease, myocardial ischemia or coronary arteriosclerosis. They can also be used in research, drug discovery forensic medicine involving angiogenesis. This sequence corresponds one of the differentially expressed proteins of the invention.
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                                                                                                            Length
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                                                                                                            Score 2364; DB 7;
Pred. No. 1.8e-188;
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100.0%; Pred. No. 1...
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09-MAY-2003; 2003JP-00131392.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                               Query Match
Best Local Similarity 100.
Matches 448; Conservative
                                                                                   Sequence 639 AA;
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The invention relates to 2495 novel polynuclectides (I) and their encoded polypeptides, sequences hybridizing to these nuclectides, sequences encoding partial polypeptides and sequences having 71% to 90% identity to the nuclectide and protein sequences. The nuclectides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a protein sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                90.9%; Score 2148; DB 8;
99.8%; Pred. No. 1.1e-170;
live 0; Mismatches 1;
           Wakamatsu A,
Otsuki T, Wakam
' v Irie R;
                                                                                                                                                  Claim 1; SEQ ID NO 3633; 2449pp; English
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                        Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity 99.8
Matches 407; Conservative
           Sugiyama T,
                            Isono Y,
                                                        WPI; 2004-535376/52
                                                                                                                                                                                                                                                                                                                                       Sequence 417 AA;
                                                                        N-PSDB; ADQ64284
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                            Yamamoto J,
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           Isogai T,
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ADK35935
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Homo sapiens

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This invention relates to a novel isolated polynucleotide comprising a nucleotide sequence selected from one of 1680 sequences, a mature protein coding portion of them, an active domain of them and thekir complementary sequences. The invention may be useful for the production of compounds with an antiarthritic, antiparkinsonian, neuroprotective, nootropic, antibacterial, antiviral, antipsoriatic, antipforiatic, antiinflammatory. In addition, the disclosed sequences may be useful for gene therapy. The polypeptides or their antibodies are useful for gene therapy. The polypeptides or their antibodies are useful for treating many diseases such as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer, psoriasis, inflammatory bowel disease and infections caused by bacteria, yourses, fungi or parasites. The present sequence is that of a human polyment of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polynucleotide encoding bone marrow derived polypeptides useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
                                                    1. .256
/label OTHER
/note= "OTHER= All Xaa's in this sequence are unknown
amino acids or the site of a stop codon within the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKQNPLPSSFPGKKITIRLAAPVCSSKTLQAEVPLSDCVQKASKPTSSTQIMVKTNMYHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 8017; 504pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treating, e.g., Parkinson's, Alzheim
disease, and inflammatory bowel disease.
                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide of the invention.
                                                                                                                                                                                                                                           05-MAR-2001; 2001WO-US004941.
                                                                                                                                                                                                                                                                              07-MAR-2000; 2000US-00519705.
                                                                                                                                                                                                                                                                                                                                                                            Liu C, Drmanac RT
                                                                                                                                                                                                                                                                                                  19-MAY-2000; 2000US-00574454
                                                                                                                                sequence"
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                                                    Misc-difference
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Human; expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coaqulation disorder; nootropic; antiallergic; antiinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide;
                                                                                                                                                                                                                                                       Zhao QA;
                                                                                                                                                                                                                                                       Zhang J,
                                                                                                                                                                                                                                                      Asundi V,
                                                                                                                                                                                                                                                       iu C, Zhou P, Asundi V,
Wehrman T, Drmanac RT;
                                                                                                                               immunostimulant; cerebroprotective.
ABP64928 standard; protein; 168 AA.
                                                                                                                                                                                                   16-NOV-2001; 2001WO-US042950.
                                                                                                                                                                                                                     17-NOV-2000; 2000US-00714936.
                                                                                                                                                                                                                                                        Liu
                                 (first entry)
                                                                                                                                                                                                                                                              Ren F, Xue AJ, Yang Y,
                                                  Human protein SEQ ID 588
                                                                                                                                                                                                                                                        Goodrich RW,
                                                                                                                                                                                                                                                                                 WPI; 2002-590824/63.
                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                         N-PSDB; ABQ99514
                                                                                                                                                                  WO200259260-A2.
                                 25-FEB-2003
                                                                                                                                                                                  01-AUG-2002.
                 ABP64928;
                                                                                                                                                                                                                                                       lang YT,
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New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity.

Claim 20; SEQ ID NO 588; 394pp; English.

The present invention relates to novel human coding sequences (ABQ99268-CABQ9608) and proteins (ABP64682-ABP65022). The sequences are useful in therappertic diagnostic and research methods. The polymucleotides may be used in the field of molecular biology as hybridisation probes, primers for PCR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The polymucleotides are useful in diagnostics as expressed sequence tags (ESTS) for identifying expressed genes or for physical mapping of the human genome. The proteins may be used as molecular weight markers, or as nuritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or pluripotential state and expand cell population in a totipotential or pluripotential state cuseful for re-engineering damaged or diseased tissues, transplantation, and expand cell population in a totipotential or pluripotential state useful for re-engineering damaged or diseased tissues, transplantation, computed to the proteins are useful for preventing, treating or ameliorating disorders involving aberrant protein expression or completed and proteins are useful for preventing, treating or anciple disorders involving aberrant protein expression or contral parterial or fungal infection, autoimmune disorders, non-healing or viral, bacterial or fungal infection, autoimmune disorders, non-healing viral, bacterial or fungal infection, autoimmune disorders, non-healing captuncleotide sequences of the invention were assembled from ESTS isolated mainly by sequences of the invention were assembled from ESTS captures obtained find not form part of the printed gasel. Note: The sequence of asset for this patent did not form part of the printed sequences obtained in electronic format directly from WIPO at the printed gasel.

282

222

Gaps ; 0 64

342

402

Sequence 168 AA;

Gaps ö 36.6%; Score 865; DB 5; Length 168; 100.0%; Pred. No. 6.4e-64; Live 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 164; Conservative

.. 0

ö 403

Gaps

; 0

9

448

셤 ò 셤 à 셤

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344 NLGEQPTKCSPEEDEEDVDDEDHDEGFGSEHELSENEEEEEEEEEDYEDDKDDDISDT
                                                                                               1 NLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHELSENEEEEEVEEDYEDVDDISDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                latency-associated nuclear antigen, LANA, gamma-2 herpes virus;
Human herpes virus 8, HHV8; rhadino virus cisa-acting element; RVCAE;
Kaposi's sarcoma; primary effusion lymphoma; PEL;
human immunodeficiency virus; HIV; multicentric Castleman's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus;
Score 557; DB 8; Length 296; Pred. No. 8.7e-38;
                                                                                                                                                                  61 FSEPGYENDSVEDLKEVISISSRKRGKRRYFWEYSEQLIPSQQER 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "nuclear localisation signal, NLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "nuclear localisation signal, NLS"
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/note= "Gln, Glu, Pro, Arg-rich region"
590. .759
                                                                                                                                               404 FSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Gln, Glu, Asp-rich region"
760. .840
/note= "Gln, Glu-rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Gln, Glu, Pro-rich region"
                                                                                                                                                                                                                                                                                                                                                                                                            Kaposi's sarcoma-associated herpesvirus LANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "acidic repeat region"
                                      0; Mismatches
                                                                                                                                                                                                                                                                                 AAY96255 standard; protein; 1162 AA
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 23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00109422
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .549
                                      Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ballestas ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14. .17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
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                                                                                                                                                                                                                                                                                                                                                        (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human herpesvirus 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-387829/33.
N-PSDB; AAA30290.
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BALL/) BALLESTAS (KAYE/) KAYE K M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIEF/) KIEFF E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200029626-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating or
                                                                                                                                                                                                                                                                                                                                                                          11-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000
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                                                                                                                                                                                                                                                                                                                      AAY96255;
 Query Match
                        Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                             RESULT 6
                                                                                                                                                                                                                                                                                 셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for ing an immune related disorder such as systemic lupus erythematosus, atoid arthritis, osteoarthritis, juvenile chronic arthritis or
                        273
                                                                                             333
                                                                                                                  rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human PRO polypeptides and the polymucleotides encoding them. The polypeptides and polymucleotides are useful for treating and disgnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, arthritis, systemic haemolytic anaemia, autoimnune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 central or peripheral nervous system, demyelinating polymeuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the
                      MVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKR
                                             1 MVKTNMYHNEKVNFHVBCKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKR
                                                                                               274 QEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; PRO; immune related disorder; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schoenfeld J, Williams PM;
                                                                                                                                                                      334 EHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEH 377
                                                                                                                                                                                           EHNYSLFVSDNLGEOPTKCSPEEDEEDVDDBDHDEGFGSEH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; SEQ ID NO 1266; 1731pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chiu H,
                                                                                                                                                                                                                                                                                                       ADO20373 standard; protein; 296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2003; 2003WO-US035268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-2002; 2002US-0425235P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO polypeptide #633
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-420067/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spondyloarthropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dennis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADO20372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004043361-A2
                                                                                                                                                                                                                                                                                                                                                                             12-AUG-2004
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WI,
                                                                                                                                    61
                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                           ADO20373;
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Ношо

RESULT

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eating or preventing a disease associated with rhodino virus infection a mammal which includes Kaposi's Sarcoma and Primary Effusion
                                                                                                                                                                                                                                                                            The present sequence is the Kaposi's sarcoma-associated herpesvirus,
                                                                                                                                                                                                    Disclosure; Fig 7; 70pp; English
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Sequence 296 AA;

Vovel

Fong Wood

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theorem and the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 NYSLFVSDNLGEQPTKCSPEEDEEDEE.-------DVDDED 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HW8; detection; diagnosis; Kaposi's sarcoma; AIDS; immunogen; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 DDEEDDEEEDEEEDEEEDEEEDEEEDDEEDNEDE-----EDDEEEDKKEDEEDGGDGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 HDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.0%; Score 190; DB 3; Length 1162;
24.2%; Pred. No. 3.4e-06;
tive 50; Mismatches 137; Indels 108; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420 -VTSISSRKRGKRRYFWEYSEQLTPSQOE 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY58500 standard; protein; 1162 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.0%
Best Local Similarity 24.2%
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1162 AA;
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10-APR-2000
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burnary Saguences AAV58480-Y58532 represent immunogenic polypeptides derived from human herpes virus type 8 (HHV8, a gammaherpesvirus). HHV8 plays an important role in the pathogenesis of ADB-related Kaposi's sarcoma. The important role in the pathogenesis of ADB-related Kaposi's sarcoma. The invention relates to a novel method of detecting the presence of human herpesvirus 8 in a biological sample using peptides representative of cominant antigenic regions of HHV8. The method comprises contacting one or more isolated, immunogenic HHV8 peptides with an antibody-containing biological sample, and detecting the formation of a complex between the peptide and the antibody. The presence of a peptide-antibody complex indicates the presence of human herpesvirus 8. The detection of HHV8 infection and be used to diagnose AIDS-associated Kaposi's sarcoma. The HVV8-specific antibodies are useful therapeutically when for the passive immunisation of a human againet HHV8 infection, thereby reducing HHV8 related disease. The detection assays are highly specific, sensitive and accurate. Early detection assays are highly specific, sensitive and accurate. Early detection and treatment of Kaposi's sarcoma could diminish the severity of symptoms related to AIDS and the sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTOSPESSORPPL-SSPTGRPDSSTPMR 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNOAGED---NGDNEISKESQVDKDD 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PQ 208
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                                                                                                                                                                                                                                                                                                                             New methods and compositions for the detection of human herpesvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.0%; Score 190; DB 3; Length 1162;
24.2%; Pred. No. 3.4e-06;
tive 50; Mismatches 137; Indels 108;
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                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 59-62; 68pp; English.
                                                                       99WO-US011407
                                                                                                                       98US-0086695P
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                                                                                                                                                                                                                                                                           WPI; 2000-097142/08
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                                                                       26-MAY-1999;
                                                                                                                         26-MAY-1998;
                       02-DEC-1999
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434 KTLSIQSSQQQQE-----PQQQEPQQQE 456

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The invention provides a composition comprising nucleic acid, histone HI protein and expression vector operationally encoding a protein suitable for tethering the nucleic acid to the histone HI protein, where the retending protein is LANA. The composition is useful in aiding the retending protein is LANA in the host cell. The viral vector encodes a protein suitable for tethering DNA to Histone HI. Methods for screening correction suitable for tethering DNA to Histone HI. Methods for screening of viral proteins to histone HI and DNA binding sites are useful for viral proteins the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis, services Huntington disease and diabetes. The present sequence represents the amino acid sequence of the Kaposi's sarcome as altigen (LANA), which acts as a tethering protein. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS-------PQ 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A composition for use in gene therapy comprises an expression vector that includes a nucleic acid sequence encoding a nucleic acid binding protein.
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                                                                                                                                                                                                   Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis;
Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8;
KSHV; latency-associated nuclear antigen; LANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.0%; Score 190; DB 4; Length 1162;
24.2%; Pred. No. 3.4e-06;
tive 50; Mismatches 137; Indels 108; Gaps
                                                                                                                                                                   Amino acid sequence of KSHV tethering protein LANA
                                     AAB62331 standard; protein; 1162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 9B; 60pp; English
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Best Local Similarity 24.2%
Matches 94; Conservative
                                                                                                             (revised)
(first entry)
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                                                                                                                                                                                                                                                                                   Human herpesvirus 8
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                                                                                                             06-AUG-2003
29-JUN-2001
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                                                                           AAB62331;
RESULT 8
                   AAB62331
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The present invention describes a system (A) for maintaining a plasmid as an episome in mammalian cells, comprising the rhadinoviral sequence LANA (latency-associated nuclear antigon) of 3489 base pairs (see ABA93487, S1) expressed in the cell, and the rhadinoviral sequence RVCAE (rhadinoviral cis-acting element) of 801 base pairs (see ABA93488, S2) present in the plasmid Also describes is a method for maintaining a closed circular DNA in a cell by expressing (S1) in the cells and having (S2) as a cis-acting and maintenance sequence in the DNA. (A) is particularly used in gene therapy (or other gene transfer applications) persistence of gene therapy wetcors in cells. The present sequence represents Kaposi's sarcoma-associated herpesvirus (KSHV, also called the present in the BNA protein, which is used in the exemplification of the present in the exemplification of the present in the mann herpesvirus (school in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the present in the exemplification of the present in the exemplification of the present in the exemplification of the present expression of the present exemplification of the pr
                                                                                                                                       --SPLPOEGPGSLAAGESSSLSASTSVSDSSOKKEEH 335
                                            269 SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   System for episomal retention of plasmids in mammalian cells, useful in gene therapy, comprises rhadinoviral LANA and RVCAE sequences.
                                                                                                                                                                                                                369 HDEGFGSEHELSENEEEEEEEDYEDDKDDISDTFSEPGYENDSVEDLKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaposi's sarcoma-associated herpesvirus; KSHV; LANA; RVCAE; PEL; KSHV terminal repeat; rhadino virus cis acting element; episome; primary effusion lymphoma; latency-associated nuclear antigen; gene therapy; gene transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaposi's sarcoma-associated herpesvirus LANA protein.
                                                                                                                                                                                                                                                                                                                            447
                                                                                                                                                                                                                                                                                                                                                                           434 KTLSIQSSQQQQE-----PQQQEPQQQE 456
                                                                                                                                                                                                                                                                                                                            420 -VISISSRKRGKRRYFWEYSEQLIPSQOE
                                                                                                              NYSLFVSDNLGEOPTKCSPEEDEEDEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB05621 standard; protein; 1162 AA
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        286 ATPALPF--KETQELLL-----
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DB 5; Length 1162;

8.0%; Score 190;

Sequence 1162 AA;

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Query Match

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14;
                                                                                                                                           238 AKVKINPVQQSRPLL----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285
                                                                                                                                                                                                                   269 SSPSEGSWGDDTAMLVILAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
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                                                                                                                 ----PQ 208
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                                                                                                                                                                                                                                                                                                           ----- 419
                                                             111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
                                                                                                                                                                      209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS 268
                                                                                        184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK
                                     124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA
            Indels 108; Gaps
                                                                                                                 163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HHV8; latency-associated nuclear antigen; LANA; primary effusion lymphoma; PEL; virucide; gene therapy; KSHV; Kaposi's sarcoma-associated herpesvirus; episome; RVCAE; rhadinovirus cis-acting element; rhadinovirus infection.
                                                                                                                                                                                                                                                                                                             369 HDEGFGSEHELSENEEEEEEEDYEDDKDDISDTFSEPGYENDSVEDLKE-
24.2%; Pred. No. 3.4e-06; ive 50; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HHV8 latency-associated nuclear antigen, LANA.
                                                                                                                                                                                                                                                                                                                                      380 DDEEDDEERDEERDEERDEERDEEDDDEDNEDE-
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99US-00298568.
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            94; Conservative
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(BALL/) BALLESTAS M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human herpesvirus 8.
 Local Similarity
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(KAYE/)
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The invention relates to an assay for determining whether a compound modulates LANA (latency-associated nuclear antigen) from KSHV (Kaposi's arcoma-associated herpesvirus, also known as HHV8, human herpesvirus 8) mediated persistence in a mammalian cell of a DNA episome having RVCAE (rhadinovirus cis-acting element) by detecting whether the compound inhibite expression of a gene resident on that episome. Also included are maintaining a closed circular DNA in a mammalian cell in which LANA is expressed (by using RVCAE as the cis-acting origin and maintenance expressed) and maintaining a plasmid as an episome in a mammalian cell (comprising: (a) Expressing LANA in the cell; and (b) having RVCAE resident on the plasmid. Compounds identified as interfering with the interaction between LANA and RVCAE are useful in treating or preventing radiant or interaction (e.g. primary effusion lymphoma (PEL)). LANA acts in trans on a 0.8 KD KSHV R(terminal repeat) unit to mediate efficient episome persistence. The present sequence represents KSHV LANA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTOSPESSORPPL-SSPTGRPDSSTPMR 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 HDEGFGSEHELSENEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE-----
                                                                                                                                                                                                                                                                                                                                                                       8.0%; Score 190; DB 8; Length 1162;
24.2%; Pred. No. 3.4e-06;
.ive 50; Mismatches 137; Indels 108;
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latency-associated nuclear antigen; tumor; viral infection;
herpesvirus type 8 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADV68154 standard; protein; 1162 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                   94; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                        Sequence 1162 AA;
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ADV68154
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11-JUL-2002; 2002US-00194046.

r compounds that modulate rhadino virus LANA action in trans on rhadino virus DNA to mediate efficient episome persistence, detecting whether the compound inhibits expression of a gene

Disclosure; SEQ ID NO 2; 28pp; English.

resident on that episome

2004-191011/18.

N-PSDB; ADJ65095

Assays for

a unit of comprises

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14;
                                                                                                                                                                                                                                                                             The invention relates to a composition comprising a latency-associated nuclear antigen (LANA) nucleic acid having any of 14 fully defined sequences of 10-61 bp given in the specification (ADV68159-ADV68172). The methods and compositions of the present invention are useful for detecting compounds that are agonistic or antagonistic for the binding of viral genetic material to genomic host DNA, in particular for detecting compounds for treating tumor and viral infections. This sequence corresponds to the LANA protein from the Kaposi's sarcoma-associated herpesvirus (also called human herpesvirus 8). The LANA protein tethers the viral DNA to the human chromosomal structural protein histone H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 SSPYQDEEVISKTPTLAQLINSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATPALPF -- KETQELLL -----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.0%; Score 190; DB 9; Length 1162;
24.2%; Pred. No. 3.4e-06;
ative 50; Mismatches 137; Indels 108; Gaps
                                                                                                                                                           New composition having a latency-associated nuclear antigen (LANA) nucleic acid, useful for detecting compounds for treating tumors and viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447
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                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 2; 51pp; English
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                99US-00410399
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                                                 (UNMI ) UNIV MICHIGAN
                                                                                                                        WPI; 2005-038492/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1162 AA;
                                                                                                                                          N-PSDB; ADV68153
                01-OCT-1999;
                                                                                      Robertson ES;
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The invention discisles a composition compitation to more insuranced factor the invention discisles or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal composed on an animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polymucleotides or their antibodies. The polymucleotide or the compound that to pain and a pharmaceutical composition comprising the one or more of polymeptides or their antibodies. The polymucleotide or the compound that complements in a setting pain and spared nerve injury (SNI) in an animal (e.g. gene for the sequence data for this patent did not form part of the printed the sequence data for this patent did not form directly from WIPO at the specification) which is differentially expressed during pain. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 KTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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1 Similarity 23.3%; Pred. No. 3.9e-06;
84; Conservative 34; Mismatches 134; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                 Costigan M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                    Befort K,
                                                                                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                               14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                                                                                                               (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                    Woolf C, D'urso D,
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                                                  Rattus norvegicus
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                                                                                                                                            255
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GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSP-----EEDEEDEE 362
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                                                                                                                        EDYEDDKDDDISDTFSE-----PGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLT
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polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating plan (e.g. spinal segmental nerve injury (thung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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1 Similarity 23.3%; Pred. No. 3.9e-06;
84; Conservative 34; Mismatches 134; Indels 109; Gaps
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence witch is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of the polynucleotide sequence which is differentially expressed in an enhant subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound of or identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more or more or more or more or more or more or more polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or the compound that preparent method for produce and that method for method for method for identifying a compound useful in treating pain and a pharmaceutical composition remaining a polypeptides or the compound that method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method for method f
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                                                                                                                                                                               New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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D'urso D,
                                                                      WPI; 2003-268312/26
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Woolf C,
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129 DEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSS 188 7.8%; Score 185.5; DB 7; Length 712; 23.3%; Pred. No. 3.9e-06; Arive 34; Mismatches 134; Indels 109; Gaps Conservative Local Similarity nes 84; Conserv Sequence 712 AA; Query Match Matches 8

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The invention discloses a composition comprising two or more isolated rat cor human polynucleotides or a polynucleotide which represents a fragment, or human polynucleotides or a polynucleotide acid sequence. Also claimed are a vector comprising the movel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence of that is differentially regulated in an animal subjected to pain and a gent to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound comprising the compound that regulates the activity of one or more of the regulates the activity in an animal of one or more of the cativity in an animal of one or more of the cativity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating cativity in an animal of one or more of the polypeptides given in the polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic compensation or mene
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                                          ADE57830 standard; protein; 712 AA.
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26-NOV-2001; 2001US-0333347P.
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84; Conservative 34; Mismatches 134; Indels 109; 7.8%; Score 185.5; DB 7; Length 712; 33.3%; Pred. No. 3.9e-06; 23.3%; Query Match Best Local Similarity Matches

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Sequence 712 AA;

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(c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-949-016-10040
US-09-248-796A-19045
US-09-418-710-21
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Maximum Match 100%
Listing first 45 summaries
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Patent No. 6657054
Patent No. 6657054
GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Regulated Anglogenesis Genes and Polypeptides
TILE REFERENCE: 1U 103 H
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 44
LENGTH: 639
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US-09-177-431-2
VCT-US-1631-2
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Best Local Similarity 100.
Matches 448; Conservative
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RESULT 3
US-09-298-568-2
Sequence 2, Application US/09298568
Fatent No. 6322792
GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: VIRUS DNA TO MEDIATE BFFICIENT BPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSGRPPL-SSPTGRPDSSTPMR 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285
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                 369 HDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE
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Pred. No. 1.4e-07;
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Best Local Similarity 24.2%;
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                                                                                                                                                                                                                                                                                                           APPLICANT: REGENAN, ISIGORE S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 112-278-0400
TELEPRAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC_DOS/W3-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
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                         TSISSRKRGKRRYFWEYSEQLTPSQQER 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                 Sequence 2, Application US/08728323A
Patent No. 5948676
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                Bohenzky, Roy A.
Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10036
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                                                                                                                                            US-08-728-323A-2
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APPLICANT:
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421
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SSPYODEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 KTLSIQSSQQQQE-----PQQQEPQQQE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 957, Application US/09538092; Patent No. 6753314; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 22.01
Matches 76; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                      PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                      163 PPPSQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS-------PQ 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
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                                                                                                                                                                                                                                                                                                                  124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
                                                                                                                                                                                                                                                                                                                                                    111 SSPIPPSHPVSPGTT----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
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Parent No. 6756203

GENERAL INFORMATION:
APPLICANT: Rieff, Elliott D.
APPLICANT: Rallestas, Mary E.
APPLICANT: Raye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: RHADINO VIRUS DATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT PAPLICATION NUMBER: US/09/894,273
CURRENT FILING DATE: 1998-11-19
PRIOR FILING DATE: 1998-11-19
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral TITLE OF INVENTION: to Genomic Host DNA FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1162
TYPE: PRT
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                                                                                                                                                                                                                                        Query Match
8.0%; Score 190; DB 2; Length 1162;
Best Local Similarity 24.2%; Pred. No. 1.4e-07;
Matches 94; Conservative 50; Mismatches 137; Indels 108;
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                                                                                                                                                                                      , ORGANISM: Kaposi's sarcoma-associated herpesvirus US-09-410-399-2
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SOFTWARE: Patentin Ver. 2.0
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TYPE: PRT
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309 GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQP-----TKCSPEEDEED 360
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                                                                                             238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285
                                                                                                                                                                                                      ATPALPP--KETQELLL----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
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                                                   184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Manafield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
CURRENT PEPLICATION WUMBER: US/09/538,092
CURRENT PILING DATE: 2000-03-29;
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CHAPPALSEGFORMATTER VERSION 0.9
SEQ ID NO 957
LENGTH: 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 706;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i LOCATION: (0)...(0)
i OTHER INFORMATION: Polypeptide Accession Number P19338
US-09-538-092-957
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321 EVKGETKSDSTTEPKVKETPKDTKEBIKTDAIVEPKVAKPIDESKODIKKDSVSAEP-KV 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----QKASKPPSSTQIMVKTNMYHNEKVNFHV-ECKDYVKKAKVKINPVQQ 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      438 VNKIEKKSGNKETMVDTKLETTLDKEVDTDSNIQEKKELFQIKEPVKDEKQIKEDLVKVE 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 TESSTDVISNTDYNDIDNSTTAETPFTELEKDTVSESLDTTTAPKTSTTNSDDDVAQLND
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                                                                                                                                                                                                                                                                                                                                         Length 709;
FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                             6.8%; Score ...
19.0%; Pred. No. 2.1e-us,
19.0%; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                           26 TLMSTDLLANSSDPDF-----MYELDREMNYQQ--
FILE OF INVENTION: FOR DIAGNOSTICS AND THER FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09047026A
Patent No. 598987
GENERAL INFORMATION:
APPLICANT: Pillus, Lorraine
APPLICANT: Clarke, Astrid
APPLICANT: Lowell, Joanna
APPLICANT: Jacobson, Sandra
                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 19.0°
Matches 115; Conservative
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Patent No. 6747137
GENERAL INFORMATION:
PAPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PELICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

WHIGH APPLICATION NUMBER: 60/231,498

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                                                                         --LSENEEEEEEEDYEDDKDD 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 2; Length 747;
1.1e-05;
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                                                                                                                                                                                             DDEDDDDEDDEEEEEEEEVKRAPGKRKKEMAKQKAAPEAKKQ 295
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                                                                                                                                                                  399 DISDTFSEPGYENDSVED---LKEVTSISSRKRGKRRYFWEYSEQ 440
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22.0%; Pred. No. 1.1e-05;
ive 52; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                  Sequence 10040, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                           361 EEDVDDEDHDEGFGSEHE
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Best Local Similarity
Matches 76; Conserv
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Sequence 21, Application US/09418710
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US-09-839-479-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 SSLSASTSVSDSSOKKEEHNY -- SLFVSDNLGEQPTKCSPEEDEEDEDVDDEDHDEGFG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 SNWEQWDTY----CEDLTKYTKLTSCDIWGTKEVDYLGLDDFSSPYQDEEVISKTPTLAQ 141
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20.6%; Pred. No. 3e-05;
tive 62; Mismatches 116; Indels 154; Gaps
       APPLICANT: Reifsnyder, Cheryl
TITLE OF INVENTION: Yeast Silencing Genes, Proteins and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,026A FILING DATE: 24-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,375
FILING DATE: 24-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REPRENCE/DOCKET NUMBER: 1-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 831 amino acids
amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                   ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                               CITY: Boulder
STATE: Colorado
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RESULT 10 US-09-418-710-21

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229 ------VECKDYVKKAK----VKI-----VKI--------NPVQQSRPLLSQIHTDAA 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 HQPNGVIQSVIQEAPLALTTKTKMQSKINENIAAASSTPFSSPVNLSTSGRRTPGNQTPV 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 GISSSDSDDLEEDBEBEEDQSIEESSEDDDSDSESBAQHKSNNQVLLHGISDPKA-DGQKAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 SRAAAPVCSSKTLQAEVPL----SDCVQKASKPPS--STQI--MVKTNMYHNEKVNFH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 MPSASPILHSQCKEK----AVSNNVNPVKTQHHSHPAKSLVEQFRGTDSDIPSSKDSED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%; Score 160; DB 2; Length 1972;
21.5%; Pred. No. 0.00014;
tive 68; Mismatches 130; Indels 146; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 PLP-----QEGP-----GGP-----GSLAAGESSSLSASTSVSDS-----
PARENTA INTERPORATION:
PREFIT NO. 6596482
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 06501-042001
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR PILING DATE: 1999-04-17
PRIOR PELICATION NUMBER: JP99-10-5
PRIOR PELICATION NUMBER: JP99-10-5
PRIOR PILING DATE: 1999-04-17
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PRESENCE FOR WINDOWS VERSION 4.0
SEQ ID NO 21
LENGTH: 1972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/09839479
Patent No. 6727222
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408 GYENDSVEDLKEVTSISS 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-09-418-710-21
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21;
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                                                                                                                                                                                                                                                                                                                          67 DIENLESFIDVLDNEGALISNWE-------QWDTYCEDLIKYIKLISCDIWGTKEV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 DYLGLDDFSSPYQDE--EVISKTPTLAQLNSEDSQSVSDSLYYPDS-LFSVKQNPLPSSF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 NY-----YONOYKKYNKSFGTTAKTESTDTDEVKDILSEDDSNILDSIXTVLSTRI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 SNNDSVT-----SQTSDI------DGLTIYEVSELTELNSLDDFVKQDLLRSKIKK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----FVSDNLGE----QP----TKCSPEEDEEDE 361
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                                                                                                                                                                                      11 PPFGDAFRS--HTFSEQTLMSTDL--LANSSDPDFMYELDREMNYQQNPRDNFLSLEDCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 PGKKITSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMY---HNEKVNFHV
                                                            6.7%; Score 157.5; DB 2; Length 738; 20.3%; Pred. No. 5.1e-05;
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21.8%; Pred. No. 0.00025;
tive 68; Mismatches 129; Indels 14
                                                                                                                             Indels
                                                                                                                             82; Mismatches 163;
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TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR FILLS REFERENCE: 06501-042001
CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-10-15
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1997-04-18
PRIOR PILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
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FastSEQ for Windows Version 4.0
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                                                                Query Match
Best Local Similarity 20.33
Matches 102; Conservative
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Matches 95; Conser
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   US-09-248-796A-16666
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Pagedence 16666 Application US/09248796A

Pagedence 16666 Application US/09248796A

Pagedence 16666 Application US/09248796A

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REFERENCE: 107196-112

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-13

PRIOR PELLOR INVERF: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409

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NAME/KEY: UNSURE
LOCATION: (154)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.8%; Score 160; DB 2; Length 1972; Best Local Similarity 21.5%; Pred. No. 0.00014; Matches 94; Conservative 68; Mismatches 130; Indels 146; Gaps
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR PEDIATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
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ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-839-479-21
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261 KENTCYCGAVAKRQEKKGME-----PLQGHATPALPFKETQE-
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256 KRKKEMAKQKAAPEAKKQ 273
                                                                                                                                                                                                                                                                                                                             410 ENDSVEDLKEVTSISS 425
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US-10-104-047-2651
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US-10-104-047-2651
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                                                                                                                                                                                                                                                                                                                                                                                                                                            179 SRAAAPVCSSKTLQAEVPL----SDCVQKASKPPS--STQI--MVKTNMYHNEKVNFH- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 EKA-----QEKRIHQPLPLAFESQTHSFQSQQKQPQVLSQQLPFIFQSSQAKEESVNKHT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VECKDYVKKAK----VKI-----NPVQQSRPLLSQIHTDAA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVIQSTGLVSNVKPLSLVNQAKKETYMKLIVPSPDVLKAGNKNTSEESSLLITSELRSKRE 236
                                                           -----VECKDYVKKAK----VKI------NPVQQSRPLLSQIHTDAA 260
                                                                                                                                      261 KENTCYCGAVAKRQEKKGME-----PLQGHATPALPFKETQE-----LLLS 301
                                                                                                                                                                                                               237 QYKQAPPSQLKKQESSKSLKKVIAALSNPKATSSSPAHP-KQTLENNHPNPFLTNALLGN 295
                                                                                                                                                                                                                                                                  302 PLP------QEGP------GSLAAGESSSLSASTSVSDS------ 328
                                                                                                                                                                                                                                                                                                      296 HQPNGVIQSVIQEAPLALTTKTKMQSKINENIAAASSTPFSSPVNLSTSGRRTPGNQTPV 355
                                                                                                                                                                                                                                                                                                                                                                   356 MPSASPILHSQGKEK----AVSNNVNPVKTQHHSHPAKSLVEQFRGTDSDIPSSKDSED 410
                                                                                                                                                                                                                                                                                                                                                                                                                      353 SPEEDEEDEEDVDDEDH-DEGFGSEHELSENEEEEER--EEDYEDDKODDISDTFSEPGY 409
63 GISSSDSDDLEEDEEEEEDQSIEESEDDDSDSESEAQHKSNNQVLLHGISDPKA-DGQKAT 121
                                     179 SRAAAPVCSSKTLQAEVPL----SDCVQKASKPPS--STQI--MVKTNMYHNEKVNFH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GLDDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKIŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.6%; Score 157; DB 2; Length 1969;
Best Local Similarity 21.8%; Pred. No. 0.00025;
Matches 95; Conservative 68; Mismatches 129; Indels 144; Gaps
                                                                                                                                                                                                                                                                                                                                           -----SOKKEEHNYSLFVSDNLG-----EQPTKC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR FILE REFERENCE: 65501-042002 CURRENT APPLICATION NUMBER: US/09/839,479 CURRENT FILING DATE: 2001-04-20 PRIOR PPLICATION NUMBER: US 09/418,710 PRIOR PILING DATE: 1999-10-15 PRIOR APPLICATION NUMBER: PCT/JP98/01783 PRIOR PILING DATE: 1998-04-17 PRIOR PILING DATE: 1997-10-24 PRIOR PILING DATE: 1997-10-24 PRIOR APPLICATION NUMBER: JP 9/310027 PRIOR PILING DATE: 1997-04-18
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6727222
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Homo sapiens
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                               296 HQPNGVIQSVIQEAPLALTIKIKMQSKINENIAAASSTPFSSPVNLSTSGRRIPGNQTPV 355
                                                                                                                                                                                                                                                                                                                                                           86 KKGATP--GKALVATPGKKG----AAIPAKGAKN---GKNAKKEDSDEEEDDDSEEDEE 135
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                                                                                                                                                                                                                                                                                                                            353 SPEEDEEDEEDVDDEDH-DEGFGSEHELSENEEBEEF--EEDYEDDKDDDISDTFSEPGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
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                                                                                                         302 PLP-----QEGP-----GSDAAGESSSLSASTSVSDS
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6.6%; Score 155.5; DB 2; Length (
Best Local Similarity 25.8%; Pred. No. 6.8e-05;
Matches 51; Conservative 34; Mismatches 70; Indels
                                                                                                                                                                                                                     329 -----SQKKEEHNYSLFVSDNLG------EQPTKC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2651, Application US/10104047
Sequence 2651, Application US/10104047
Patent No. 6943241
GENERAL INPORMATION:
FALEN PELICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE:
PRIOR FILING DATE:
NUMBER OF SEQ 1D NOS: 4096
SOSTWARE: PATENTIN VET. 2.1
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Job time : 40.7997 secs
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Sequence 2651, Applisequence 7, Applisequence 1332, Ap Sequence 52482, Ap Sequence 1, Applisequence 1280, Ap Sequence 2637, Applisequence 313, Applisequence 313, Applisequence 3126, A Sequence 3126, A Sequence 2513, Applisequence 3126, A Sequence 23513, Applisequence 3126, A Sequence 23513, Applisequence 3114, A Sequence 3114, A Sequence 3114, A Sequence 3114, A Sequence 31314,  OM protein

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Sequence:

Searched:

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Result No.

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SLEDCKDIENLESFTDVLDNEGALTSNWEGWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SLEDCKDIENLESFTDVI, DNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLPQEGPGSLAAGESSSLSASTSVSDSSQXKEEHNYSLFVSDNLGEQPTKCSPEEDEED 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFWYELDREMNYQONPRDNFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44, Application US/10717665

Sequence 44, Application US/20050106579A1

GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc
APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/717,665
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/10/164,595
PRIOR APPLICATION NUMBER: US/10/164,595

PRIOR FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2364; DB 5;
100.0%; Pred. No. 9.4e-153;
iive 0; Mismatches 0;
US-10-104-047-2651

US-11-013-684-7

US-10-408-763-1332

US-10-408-763-1332

US-10-408-763-1280

US-10-408-763-1280

US-10-408-763-1280

US-10-450-763-46978

US-10-450-763-46978

US-11-097-143-30126

US-10-978-242-3

US-10-779-543-23513

US-10-779-543-23513

US-11-097-143-3014

US-11-097-143-3014

US-11-097-143-3014

US-11-097-143-3014

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US-11-057-143-3014

US-11-057-143-3014
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Matches 448; Conservative
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CRGANISM: Homo sapiens
US-10-717-665-44
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Sequence 19, Appl
Sequence 169, Appl
Sequence 41629, A
Sequence 34710, A
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37245, A
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APPLICANT: Kieff, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: RAP.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE TILE REPERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/109,422
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   361 EEDVDDEDHDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKEV
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Sequence 3319, Application US/10732923

Sequence 3319, Application US/10732923

Sequence 3319, Application US/20050108791A1

GENERAL INFORMATION:

TTILE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

TTILE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT PILING DATE: 2003-12-10

PRIOR PELING DATE: 2003-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 3319
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                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-10-732-923-3319
                                                               TSISSRKRGKRYFWEYSEQLTPSQQER
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APPLICANT: Robertson, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA FILLE REPRENCE: UM-03778
CURRENT APPLICATION NUMBER: US/10/294,804
CURRENT PILLING DATE: 2002-11-14
PRIOR FILLING DATE: 1999-10-01
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                                                                                                                                                                                 Length 1162;
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ORGANISM: Kaposi's sarcoma-associated herpesvirus
                                                                                                                                                                               8.0%; Score 190; DB 3; I
24.2%; Pred. No. 0.00043;
tive 50; Mismatches 137;
                                                                                                              ORGANISM: Kaposi's sarcoma-associated herpesvirus
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Publication No. US20030133948A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                 94; Conservative
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Matches 94; Conser
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293 KETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNY-----SLFVSDNL 345
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GENERAL INFORMATION;
APPLICANT: RICHARDSON, Thomas W.; WARREN, Bridget A.;
APPLICANT: RICHARDSON, Thomas W.; WARREN, Bridget A.;
APPLICANT: GRIFFIN, Jennifer A.; TANG, Y. Tom;
APPLICANT: VUE, Henry; BAUGHN, Mariah R.;
APPLICANT: EMERLING, Brooke M.; FORSYTHE, Ian J.;
APPLICANT: BUND Aina M.; FORSYTHE, Ian J.;
APPLICANT: RAMKUMAL, Jayalaxmi; LI, Joana X.;
APPLICANT: BURFORD, Neil, ELLIOTT, Vicki S.;
APPLICANT: BURFORD, Neil, ELLIOTT, Vicki S.;
APPLICANT: BOROWSKY, Mark L.; YAO, Monique G.;
APPLICANT: BOROWSKY, Mark L.; YAO, Monique G.;
APPLICANT: WALIA, Narinder K.; HAFALIA, April J. A.;
APPLICANT: WALIA, Narinder S.
TITTE OF INVENTION: UNUCLEIC ACID-ASSOCIATED PROTEINS
FILE REFERENCE: PP-1068 USN
CURRENT FILING DATE: 2004-12-12
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24.5%; Pred. No. 0.006;
tive 44; Mismatches 120;
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7037554CD1
US-10-483-505-3
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CURRENT FILING DATE: 2004-12-12
RICOR APPLICATION NUMBER: PCT/USO2/21971
PRIOR PILING DATE: 2002-07-10
PRIOR PELING DATE: 2001-07-12
PRIOR PILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
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PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-19
PRIOR PILING DATE: 2001-07-19
PRIOR PILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-27
                                                                                                                                                                                                                                                                   Sequence 3, Application US/10483505
Publication No. US20050118582A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 86; Conserva
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                                                                                                                                                    ----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285
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24.2%; Pred. No. 0.00043;
tive 50; Mismatches 137; Indels 108;
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TITLE OF INVENTION: LANA Viral Protein Binding Sites
FILE REPERENCE: UM-07142
CURRENT APPLICATION NUMBER: US/10/194,046
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: 09/410,399
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
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ORGANISM: Kaposi's sarcoma-associated herpesvirus
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                                                                                                                                                         238 AKVKINPVQQSRPLL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.2%
Matches 94; Conservative
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; Sequence 19, Application US/10400083; Publication No. US20040186056A1; GENERAL INFORMATION:
                    Sequence 3, Application US/10384569 Publication No. US20040002457A1 GENERAL INFORMATION:
                                                                                        APPLICANT: HOVANESSIAN, ARA G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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                                                                                                   195 GNNTENEEEGVEEDVEEDEEVEEDAEBDERVDEDGER--EBEBEBEBEBEBEBEBEBEYBQ 252
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APPLICANT: HOVANGESIAN, ARA
APPLICANT: Callebaut, Christian
APPLICANT: Callebaut, Christian
APPLICANT: Callebaut, Christian
APPLICANT: Waller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Briand, Jean-Paul
APPLICANT: Guichard, Glan-Paul
PRIOR APPLICATION NUMBER: US/09/825,886
CURRENT FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/EP98/01409
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1997-03-12
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 22
LENGTH: 707
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G-----EQPTKCSPEEDEEDVD-----DEDHDEGFGSEHELSENEEEEEEDVED 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 KN---GKNAKKEDSDEEEDDDSEEDEEDDEDEDEDEIEPAAMKAAAAAPASEDEDDED 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 DPKKMAPPPKEVEEDSEDEEDSEDE--EDDS--SGEEVVIPOK-KGKKAAATSAKKVVVS
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                                                                                                                                                           395 DKDD------DISDTFSEP-GYENDSVEDLKEVTSISSRKRGKRR 432
                                                                                                                                                                                       Query Match 7.0%; Score 165; DB 3; Length 707; Best Local Similarity 22.0%; Pred. No. 0.012; Matches 76; Conservative 52; Mismatches 123; Indels
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                                                                                                                                                                                                                                                                                                                  ; Sequence 22, Application US/09825886; Publication No. US20020076693A1
; GENERAL INFORMATION:
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US-09-825-886-22
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RESULT

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APPLICANT: BRIAND, JEAN-PAUL
TITLE OF INVENTION: INHIBITION OF VIRUS ANCHORAGE BY RGG DOWAIN OF A CELL SURFACE-
TITLE OF INVENTION: INHIBITION PROTEIN, POLYNUCLEOTIDE CODING FOR SAID RGG DOWAIN,
TITLE OF INVENTION: EXPRESSED PROTEIN, POLYNUCLEOTIDE CODING FOR SAID RGG DOWAIN,
TITLE OF INVENTION: PROTEIN LIGAND BINDING TO THE CELL-SURFACE-EXPRESSED PROTEIN
FILLE REFERENCE: 0.945.0260-00000
CURRENT APPLICATION NUMBER: US/10/384,569
CURRENT PILING DATE: 2004-07-14
PRIOR PLILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/383,371
PRIOR APPLICATION NUMBER: 60/383,371
PRIOR APPLICATION NUMBER: 60/383,371
PRIOR APPLICATION NUMBER: 2002-03-12
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.1
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APPLICANT: Rucelaliti, Erkki
APPLICANT: Rucelaliti, Stem
APPLICANT: Porkka, Kimmo
APPLICANT: Christian, Sven
TITLE OF INVENTION: HARN Selectively Home to Tumor Blood Vessels and Tumor Cells
TITLE OF INVENTION: LAS Selectively Home to Tumor Blood Vessels and Tumor CILE
FILIS REFERENCE: PLL 562
CURRENT APPLICATION NUMBER: US/10/400,083
CURRENT FILING DATE: 2003-03-20
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: EastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.0%; Score 165; DB 4; Length 70 Best Local Similarity 22.0%; Pred. No. 0.012; Matches 76; Conservative 52; Mismatches 123; Indels
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LOCATION: (117)...(167)
CTHER INFORMATION: Neuromodulin (GAP-43) proteins domain identified by eMATRIX,
OTHER INFORMATION: accession number BL00412D, p-value=8.644e-15, raw score of 16.54
US-10-450-763-41629
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---KAAATPAKKTVTPAK-- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 SOKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHELSENEEEEE
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                                                  249 RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGP
                                                                                                                                            309 GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQP-----TKCSPEEDEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Sequence 41629, Application US/10450763
| Sequence 41629, Application Wo/10450763
| Publication No. US20050196754A1
| GENERAL INFORMATION:
| APPLICANT: Hyseq, Inc
| TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
| FILE REPERENCE: 790C1P3/US
| CURRENT APPLICATION NUMBER: US/10/450, 763
| CURRENT APPLICATION NUMBER: US/10/6831
| PRIOR APPLICATION NUMBER: 09/540, 217
| PRIOR PILING DATE: 2000-03-30
| PRIOR PILING DATE: 2000-03-31
| PRIOR PILICATION NUMBER: 09/649, 167
| PRIOR PILICATION NUMBER: 09/649, 167
| PRIOR PILING DATE: 2000-03-31
| PRIOR PILING DATE: 2000-03-31
| NUMBER OF SEQ ID NOS: 60736
| SEQ ID NO 41629
| LENGTH: 167
                                                                                                                                                                                                                                                                                                                                               399 DISDIFSEPGYENDSVED---LKEVTSISSRKRGKRRYFWEYSEQ 440
                                                                                                                                                                                                                                                                                                                                                                             ch 6.9%; Score 162; DB 5; Length 16
1 Similarity 30.5%; Pred. No. 0.0029;
46; Conservative 28; Mismatches 55; Indels
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; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyeer, INC.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 EEDYEDDKDDDISDTFSEPGYENDSVEDLKE 419
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       68 PT--KKVAVATPAKKAAVTPGK-
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Matches 46; Conserva
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NAME/KEY: DOMAIN
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                                                                                                      103 ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 KTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS 248
                                                                                                                                                                                                                                                                                                                                            PT--KKVAVATPAKKAAVTPGK-------KAAATPAKKTVTPAK- 102
                                                                                                                                                                                                                                                                                                                                                                                                   249 RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQP-----TKCSPEEDEED 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 KN---GKNAKKEDSDEEEDDDSEEDEEDEDEDEDEDEDETEPAAMKAAAAPASEDEDDED 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LSENEEEEEEDYEDDKDD 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                -----AVTTPGKKGATP--GKALVATPGKKG----AAIPAKGA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pardo, Jorge
APPLICANT: Abao, Haoran
APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: Modulators of Lymphocyte Activation and Migration
FILE REFERENCE: 02104-00033005
CURRENT APPLICATION NUMBER: US/10/491,545A
CURRENT FILING DATE: 2004-04-01
                                                                                                                                                      94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.0%; Score 165; DB 5; Length 707; Best Local Similarity 22.0%; Pred. No. 0.012; Matches 76; Conservative 52; Mismatches 123; Indels
                                                                                                           DB 4; Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               399 DISDIFSEPGYENDSVED---LKEVISISSRKRGKRRYFWEYSEQ 440
                                                                                                           7.0%; Score 165; DB 4; Length 70° 22.0%; Pred. No. 0.012; trive 52; Mismatches 123; Indels
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PRIOR PLING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: WO PCT/US02/31618
PRIOR FILING DATE: 2002-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: human nucleolin (NCL) US-10-491-545A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/10491545A Publication No. US20050130117A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 EEDVDDEDHDEGFGSEHE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chu, Peter
APPLICANT: Li, Congfen
APPLICANT: Liao, X. Charlene
APPLICANT: Masuda, Esteban
                                                                                  Query Match
Best Local Similarity 22....
Best Local Conservative
76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 20
LENGTH: 707
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                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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                                                                 US-10-400-083-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 CDIWGTKEVDYLGLDDFSSPYQDEEVISKTPT--LAQLNSEDSQSVSDSLYYPDSLFSVK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 HTDAAKENTCYCGAVAKRQEKKGMEPLQ-----GHATPALPFKETQELLLSPLPQEGPG 309
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                                                                                                                                                                                                                                                                                                                                             DB 4; Length 1974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Mismatches 152;
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; Publication No. US20020039779A1
; GENERAL INPORMATION:
    APPLICANT: Jones, Michael H.
    TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
    FILE REFERENCE: 66501-04200
    CURRENT APPLICATION NUMBER: US/09/839,479
    CURRENT FILING DATE: 2001-04-20
    FRIOR PELICATION NUMBER: US 09/418,710
    FRIOR PLING DATE: 1999-10-15
    FRIOR PLING DATE: 1999-04-17
    FRIOR APPLICATION NUMBER: UP 9/310027
    FRIOR PLING DATE: 1998-04-17
    FRIOR APPLICATION NUMBER: UP 9/310027
    FRIOR PLING DATE: 1997-04-18
    FRIOR PLING DATE: 1997-04-18
    FRIOR FILING DATE: 1997-04-18
    FRIOR FILING DATE: 1997-04-18
    NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                    No. 0.088;
                                                                                                                                                                                                                                                                                                                                             6.8%; Score 160.5;
21.6%; Pred. No. 0.08
           60/360,039
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                                                                                                                                                                                                TYPE: PRT ORGANISM: Caenorhabditis elegans
   PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5455
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 104; Conservative
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LENGTH: 1972
                                                                                                                                                                LENGTH: 1974
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NAME/KEY: DOMAIN
LOCATION: (308)...(343)
OTHER INFORMATION: Matrix protein (MA) p15. domain identified by eMATRIX,
OTHER INFORMATION: accession number PF01140D, p-value=2.570e-09, raw score of 15.54
US-10-450-763-34710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-10-369-493-5455
5 Sequence 5455, Application US/10369493
5 Publication No. US20030233675A1
6 GENERAL INFORMATION:
7 APPLICANT: Cao, Yongwei
7 APPLICANT: Glegory J.
8 APPLICANT: Clen, Xianfeng
7 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
8 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
9 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
9 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
9 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
9 CURRENT APPLICATION NUMBER: US/10/369,493
9 CURRENT PILING DATE: 2003-02-28
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                                   CURRENT FILLING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PILLING DATE: 2001-03-30
PRIOR PELICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR PILLING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
CURRENT APPLICATION NUMBER: US/10/450,763 CURRENT FILING DATE: 2003-06-11
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                                                                                                                                        179 SRAAAPVCSSKTLQAEVPL----SDCVQKASKPPS--STQI--MVKTNMYHNEKVNFH- 228
                                                                                                                                                                                                    -----VECKDYVKKAK----VKI-----NPVQOSRPLLSQIHTDAA 260
                                                                                                                                                                                                                                                                                                                 KENTCYCGAVAKROEKKGME-----PLOGHATPALPFKETOE------LLLS 301
                                                                                                                                                                                                                                                                                                                                                                                  302 PLP-----QBGP----- 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.9 -----SQKKEEHNYSLFVSDNLG-----EQPTKC------352
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                                                5.8%; Score 160; DB 3; Length 1972;
Similarity 21.5%; Pred. No. 0.095;
94; Conservative 68; Mismatches 130; Indels 146; Gaps
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CURRENT APPLICATION NUMBER: US/09/418,710
PRIOR APPLICATION NUMBER: US/09/418,710
PRIOR RILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR PILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR RILING DATE: 1997-04-18
PRIOR RILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FASISEQ for Windows Version 4.0
LENGTH: 1972
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                                              Query Match
Best Local Similarity 21.5*
Matches 94; Conservative
; ORGANISM: Homo sapiens
US-09-839-479-21
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179 SRAAAPVCSSKTLQAEVPL----SDCVQKASKPPS--STQI--MVKTNMYHNEKVNFH-
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38, Appl 2, Appli 6, Appli 6, Appli 351, App 200, App 2987, Ap 10232, A 4, Appli 8, Appli 8, Appli 4, Appli 4, Appli 529, Appli 529, Appli 35, Appli

Sequence:

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APPLICANT: INSTITUT PASTEUR
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APPLICANT: INSTITUT PASTEUR
APPLICANT: INSTITUT PASTEUR
TITLE OF INVENTION: IDENTIFICATION OF A CONSERVED REGION OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: MSP3 TARGETED BY BIOLOGICALLY ACTIVE ANTIBODIES
FILE REFERENCE: 275601US0
CURRENT PAPPLICATION NUMBER: US/11/189,817
PRIOR FILING DATE: 2005-07-27
PRIOR FILING DATE: 2004-08-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATCHIN VERSION 3.3
SOFTWARE: PATCHIN VERSION 3.3
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I Similarity 20.9%; Pred. No. 0.00034;
82; Conservative 61; Mismatches 146; Indels 104; Gaps
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US-10-530-340-14
US-11-097-728-2
US-11-097-728-6
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US-10-485-517-351
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US-11-072-512-2987
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US-11-138-642-4
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US-11-189-817-2
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Sequence 2651, Appli
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556.876 Million cell updates/sec
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                                             GenCore version 5.1.7
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US-11-124-3661-1
US-11-124-367A-293
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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13

349 PTKCSPEEDEEDVDDEDHOEGFGSEHELSENEEEEEEEDVEDDKODDISDTFSEPG 408

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196 KKAAKVVPVKAKNVAEDEDEEEEDEEDEDEDDDDEDDEEDDEEEEEEEFFFFFF 255
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APPLICANT: Honglin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.0RD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR APPLICATION NUMBER: US 60/569,609
PRIOR PILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
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CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR PLING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 293, Application US/11124367A Publication No. US20060024700A1 GENERAL INFORMATION:
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                                  OTSUKI, TETSUJI
WAKANATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAMECHIKA, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                   NAGAI, KEIICHI
IRIE, RYOTARO
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Matches 51; Conserva
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APPLICANT:
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Publication No. US20060024324A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Vaccines comprising chimeric malaria proteins derived from Plasmo TITLE OF INVENTION: falciparum
TITLE OF INVENTION: falciparum
TITLE OF INVENTION: falciparum
CURRENT APPLICATION NUMBER: US/11/128,660
CURRENT FILING DATE: 2005-05-12
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 651
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                                                                                                                                                               | | : | : | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                   409 YENDSVEDLKEVTSISSRKRGKRRYFWEYSEQL 441
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Sequence 2651, Application US/11072512 Publication No. US20060029945A1 GENERAL INFORMATION: APPLICANT: ISOGAI, TAKAO

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391 RLDEVISKYAMLQDKSEBGERKKRRARLQGTSSHS---ADTPEASLD--SGEGPSGMASQ 445
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                        210 STQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKEN----
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Pred. No. 0.042;
0; Mismatches 50;
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CURRENT APPLICATION NUMBER: US/11/054,281
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: 60/261,014
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR FILING DATE: 2001-01-11
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i. Sequence 107, Application US/11054281
i. Publication No. US20060013813A1
i. GENERAL INFORMATION:
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US-11-054-281-107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TCYCGAVAKROE---KKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAA- 313
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Subjication No. US20060024700A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: Michele Cargill
APPLICANT: Michele Cargill
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APPLICANT: Michele Cargill
FILE REFERENCE: CLOOUS19, ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT APPLICATION NUMBER: US 60/568,846
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR PILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/589,554
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-09
SOFTWARE: FESTERG for Windows Version 4.0
SEQ ID NO 292
LENGTH: 760
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6.4%; Score 150.5; DB 7; Length
Best Local Similarity 23.1%; Pred. No. 0.0059;
Matches 83; Conservative 55; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                              6.4%; Score 150.5; DB 7;
23.1%; Pred. No. 0.0058;
                                                                                                                                                                                                                                                                                                                                               55; Mismatches 142;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.11
Matches 83; Conservative
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ORGANISM: Homo
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                                SEQ ID NO 293
LENGTH: 740
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        582 LPAQVGTIMDSSYSANROVFFOSVADKEAIANFTNOKNISNPPDMSG------WNPFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.9%; Score 140; DB 6; Length 1168; Best Local Similarity 19.3%; Pred. No. 0.05; Matches 90; Conservative 55; Mismatches 136; Indels 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEEE----DYEDDKD--DDISDTFSEPGYENDSVEDLKEVTSISSR 426
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       Sequence 1. Application US/10509422;
Publication No. US20050244825A1
GENERAL INFORMATION:
TTILL OF INVENTION:
TTILL OF INVENTION:
TTILL OF INVENTION:
TILL REFERENCE: 004974.01015;
CURRENT APPLICATION NUMBER: US/10/509,422
CURRENT FILING DATE: 2004-09-24;
PRIOR FILING DATE: 2003-03-20;
PRIOR FILING DATE: 2002-03-27;
PRIOR APPLICATION NUMBER: US 60/406,936;
PRIOR FILING DATE: 2002-03-27;
PRIOR APPLICATION NUMBER: US 60/406,936;
PRIOR FILING DATE: 2002-03-37;
PRIOR FILING DATE: 2002-03-37;
PRIOR FILING DATE: 2002-03-37;
PRIOR FILING DATE: 2002-03-37;
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PRIOR FILING DATE: 2002-03-37;
PRIOR APPLICATION NUMBER: US 60/406,936;
PRIOR FILING DATE: 2002-03-37;
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PRIOR DATE: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1168
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-509-422-2
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ITILE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REPRENCE: 21402-240CIP

CURRENT APPLICATION NUMBER: US/11/054,281

CURRENT FILING DATE: 2005-02-08

PRIOR APPLICATION NUMBER: 60/261,014

PRIOR PLING DATE: 2001-01-11

PRIOR PLING DATE: 2001-01-11

PRIOR PLING DATE: 2001-01-11

PRIOR PLING DATE: 2001-01-11

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PRIOR PLING DATE: 2001-01-11

PRIOR PLING DATE: 2001-01-11

PRIOR PLING DATE: 2001-01-11

PRIOR PLING DATE: 2001-08-17

PRIOR PLING DATE: 2002-01-11

PRIOR PLING DATE: 2002-01-11
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5.9%; Score 138.5; DB 6
Best Local Similarity 30.5%; Pred. No. 0.0053;
Matches 32; Conservative 20; Mismatches 28
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CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: DE SEQ Genes Version 1.0
SEQ ID NO 1254
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US-11-054-281-108
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; ORGANISM: Homo sapiens
US-10-821-234-1254
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Best Local Similarity
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; ORGANISM: Homo sapiens
US-11-054-281-106
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Matches 51; Conserv
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LENGTH: 1735
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US-10-495-083-3
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APPLICANT:
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US-LI-054-281-28

| Jeduance 28, Application US/11054281
| Jebblication No. US20060013813A1
| JEDBREAL INFORMATION:
| APPLICANT: Mezes et al.
| TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REPERBRES: 21402-240CIP
| TITLE OF INVENTION PROPER: US/11/054,281
| CURRENT FILING DATE: 2005-02-08
| PRIOR PLICATION NUMBER: 60/261,018
| PRIOR FILING DATE: 2001-01-11
| PRIOR FILING DATE: 2001-01-11
| PRIOR FILING DATE: 2001-01-11
| PRIOR FILING DATE: 2001-09-10
| PRIOR FILING DATE: 2001-01-11
| PRIOR FILING DATE: 2001-01-11
| PRIOR FILING DATE: 2001-01-11
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| PRIOR FILING DATE: 2001-01-11
| PRIOR FILING DATE: 2001-01-11
| PRIOR PRIOR PRICATION NUMBER: 60/313,170
| PRIOR PRIOR DATE: 2001-01-11
| PRIOR PRIOR DATE: 2001-01-11
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SOFTWARE: PatentIn Ver. 2.1
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TITLE OF INVENTION: UNC-13 IN THE MODULATION OF NEUROTRANSMISSION AND SECRETION EVENTE FILE REFERENCE: 009848-0309442
CURRENT APPLICATION NUMBER: US/10/495,083
CURRENT FILING DATE: 2004-05-05
PRIOR PILING DATE: 2002-10-29
PRIOR FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: EP 01 12 6235.9
PRIOR FILING DATE: 2001-11-05
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29.0%; Pred. No. 0.06
tive 35; Mismatches
PRIOR APPLICATION NUMBER: 60/201,02.
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/313,170
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 10/044,564
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.1
SSEQ ID NO 106
LENGTH: 1219
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SOFTWARE: PatentIn version 3.1
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ASHERY, Uri
JUNGE, Harald
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US-11-124-367A-433
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Publication No. US20050266242A1
GENERAL INFORMATION:
APPLICANT: Lindquist et al.
TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
FILE REPERENCE: 30554/40025A
CURRENT APPLICATION NUMBER: US/11/089,551A
PRIOR APPLICATION NUMBER: US 60/559,286
PRIOR APPLICATION NUMBER: US 60/559,286
PRIOR FILING DAIE: 2004-03-31
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 305, Application US/11124368A

Publication No US20050287559A1

GENERAL INFORMATION:

APPLICANT: James J. Devlin

APPLICANT: James J. Devlin

APPLICANT: James J. Devlin

APPLICANT: James J. Devlin

APPLICANT: Michele Cargill

APPLICANT: James J. Devlin

APPLICANT: James J. Devlin

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

CURRENT APPLICATION NUMBER: US/11/124,368A

CURRENT FILING DATE: 2005-05-09

PRIOR APPLICATION NUMBER: US 60/568,845

PRIOR APPLICATION NUMBER: US 60/568,945

PRIOR APPLICATION NUMBER: US 60/655,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 SLAAGESSSISASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDVDDEDH 369
                                                                                                                                                                                       247
                                                                                                                                                                                                                         276 KKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
                                                                                                                                                                                                                                                                                                          336 NYSLFVSDNLGEQPT-----KCSP--EEDEEDEEDVDDEDHDEGFGSEHELSE- 381
                                                                                                                                                                                                                                                                                                                                   285 SLQGSELDDERDRDSYHSCHSSVSYHKDSPRWDQDEEDLEDLE-DEELD-DEELERB 343
                                                                                                   ----VPSSQCCNWNYFGWGEQNDDPDSA-VDDRDSDY 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 DEGFGSEHELSENEEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKEVTSISSRK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 TFHRILLDAHFELPLDIPEEEARYWAKKLEQLNAARDQDEYSFQDQ------QDKP
                                                                                                                                                                                 201 RSETSNSIPPPYYTTSQPNASVHQYSVRP----PPLGSR------ESYSDSMHSYEE
                                                             LPSSFPGKKITSRAAAPVCSSKTLQAEVPLSDCVQ-----KASKPPSSTQIMVKTNMY
                                                                                                                                                                                                                                                                   -----FSEPR--ALSP----TGSSRYASSGELSQGSSQLSEDFDPDEH
                                                                                                                                             221 HNEKVN-----FHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 414;
                                                                                                                                                                                                                                                                                                                                                                                              382 --NEEEEEEEEDYEDDKDDISDTF-SEPGYENDSVEDLKEVTSIS 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Indels
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5.7%; Score 134; DB 7;
Best Local Similarity 30.5%; Pred. No. 0.037;
Matches 36; Conservative 25; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Saccharomyces cerevisiae US-11-089-551A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 414
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US-11-089-551A-28
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2293 ETTDADKEPAGE---DKGIKALKESAKOTPAPAASVTGSRRRPRAPRESAQAIEDLAGFK 2349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1935 PKPAVS------DEKNINTFVETPVQKLDLLCN------LPGSKRQPQTPKEKAEA 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 LPQEGPGSLAAGESSSL---SASTSVSDSSQKKEEHNYSLFVSDNLGEQP----TKCSP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 EEDBEDEEDVDDEDHDEGF------GSEHELSENEBEBEBEBDXEDDK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION WHERE: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION WHERE: US 60/569,846
PRIOR APPLICATION WHERE: US 60/582,609
PRIOR APPLICATION WHERE: US 60/582,609
PRIOR PILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-06-25
PRIOR SPECIATION WHERE: US 60/599,554
PRIOR SEQ ID NOS: 34460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 433
LENGTH: 2801
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                      2 PQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFWYELDREMNYQQNPRDNFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1979 LEDLVGFKELFQTPGHTEESMIDDKITEVSCKSPQPESFKISRSSKQRLKIPLVKVDMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 DLTKYTKLT-----SCDIWGTKEVDYLGLDDFSSPYQD-BEVISKTPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SPKQILDPAASVTGSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 AQLNS--EDSQSVSDSLYYPDSLFSV-----KQNPLPSSFPGKKITSRAAAPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || :| | ::| | :| | 2089 RQIRTERSMTIDKNTKIPCKSPPPELTDTAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 SSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 QS----RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.6%; Score 132.5; DB 7; Length 2801; 20.8%; Pred, No. 0.46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 LEDCKDIENL-----ESFTDVLDNEGALTS-NWEQWDT
                                                                                                                                                                                                                                                                                          ; Pred. No. 0.46;
65; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2039 EPLAVSKLTRISGETTQTHTEPTGDSKSIKAFKE
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 305
LENGTH: 2801
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                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 20.8%
Matches 110; Conservative
                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens US-11-124-367A-433

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2039 EPLAVSKITRTSGETTQTHTEPTGDSKSİKAFKE-----SPKÖILDPAASVTGSR 2088
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                                                                                                                                                                                                     -----SCDIWGTKEVDYLGLDDFSSPYQD-EEVISKTPTL 139
                                                                                                                                                                                                                                                                                                                                         187 SSKTLOAEVPLSDCVOKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 LPQEGPGSLAAGESSSL---SASTSVSDSSQKKEEHNYSLFVSDNLGEQP----TKCSP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 EEDEEDBEDVDDEDHDEGF------GSEHELSENEEEEEBEBÜNK 396
                                                                                                                                                                                                                                                                        140 AQLNS--EDSQSVSDSLYYPDSLFSV------KQNPLPSSFPGKKITSRAAAPVC 186
                                                                                                                                                                                                                                                                                                                                                                                                         247 QS----RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSP 302
                                                                  2 POPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFLS 61
                                                                                                                                   62 LEDCKDIENL------YCE 96
Query Match 5.6%; Score 132.5; DB 7; Length 2801; Best Local Similarity 20.8%; Pred. No. 0.46; Matches 110; Conservative 65; Mismatches 184; Indels 169; Gaps
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Search completed: February 28, 2006, 09:02:40 Job time : 13.9766 secs

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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                   Copyright
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OM protein - protein search, using sw model

Run on:

February 28, 2006, 08:45:35; Search time 27.3216 Seconds (without alignments) 1577.691 Million cell updates/sec

US-10-717-665A-44_COPY_1_448

2364 1 MPQPSVSGMDPPFGDAFRSH.....GKRRYFWEYSEQLTPSQQER 448 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*

Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Match Length	B	OI OI	Description
	188.5	8.0	707	-	DNMS	nucleolin - mouse
7	185.5	7.8	712	7	JH0148	nucleolin - rat
٣	178.5	7.6	2761	7	T29285	hypothetical prote
4	165	7.0	678	7	A54514	glutamic acid-rich
Ŋ	165	7.0	707	7	A35804	_
v	162	6.9	1187	7	T46637	₽
7	161	6.9	831	~	S39835	hypothetical prote
ω	160.5	6.8	1974	~	T16703	
6	159.5	6.7	1128	~	G86266	hypothetical prote
10	157	9.9	562	~	S38149	
11	153	6.5	792	7	T42963	hypothetical prote
12	152.5	6.5	200	7	S55785	nucleolar protein
13	152.5	6.5	968	~	T24169	hypothetical prote
14	152.5	6.5	906	~	T24166	
15	152	6.4	1038	~	S52522	hypothetical prote
16	152	6.4	1182	N	T30189	myelin transcripti
17	151.5	6.4	740	~	T03847	
18	151.5	6.4	1188	~	T46608	zinc finger protei
19	150.5	6.4	669	N	T01029	_
20	150.5	6.4		0	A27441	nucleolin - Chines
21		6.4	797	0	A36811	hypothetical prote
22	149	6.3	1063	~	A40253	acidic nuclear pro
23	149	6.3	1262	7	T33074	hypothetical prote
24	148.5	6.3	1089	~	S48244	NMD2 protein - yea
	148.5	6.3	1094	N	S49313	protein kinase - s
	148.5	6.3	1300	~	T03166	probable immediate
27	148	6.3	972	N	T49773	related to actin-i
	147	6.2	3724	7	T18427	U
29	146.5	6.2	727	~	JC5113	ribosomal transcri

F;397-402/Region: RNA-binding RNP2 motif F;431-438/Region: RNA-binding RNP1 motif F;488-551/Domain: ribonucleoprotein repeat homology <RRM3> F;489-494/Region: RNA-binding RNP2 motif

ribosomal transcri	nestin - golden ha	nucleolin - chicke	transcription fact	neurofilament prot	fibrinogen-binding	immediate-early pr	hypothetical prote	probable transcrip	IFH1 protein - yea	hypothetical prote	probable secreted	transcription acti	probable TPR repea	ASF1 protein - yea	transcription init
JC5112	T34518	DNCHNL	S17196	T52485	S41539	EDBEQ3	T15094	T38274	S55352	E86336	A71623	T30967	B84476	330766	S37845
~	N	-	N	'n	7	Н	~	0	N	~	7	~	0	7	7
764	1804	694	701	913	933	407	553	990	1085	409	1192	1100	1115	279	482
6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.1	6.1	6.1	6.1	6.0	6.0	6.0	6.0
146.5	146.5	146	146	146	146	145.5	145.5	145	145	144.5	144.5	143	143	142.5	142
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mas musculus (special special spe
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A; Residues: 2-20, "X, 22-24 «PAS>
A; Cross-references: UNIPARC: UPI00001739CF
R; Yang, T.H.; Tsai, W.H.; Lee, Y.M.; Lei, H.Y.; Lai, M.Y.; Chen, D.S.; Yeh, N.H.; Lee, S.
Mol. Cell: Biol. 14, 6068-6074, 1994
A; Title: Purification and characterization of nucleolin and its identification as a trans
A; Reference number: A56240; MUID: 94344117; PMID: 8065340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT: P09405; UNIPARC:UPI0000009C3; GB:X07699; NID:g53453; PIDN:C; R;Pasternack, M.S.; Bleier, K.J.; McInerney, T.N. J. Biol. Chem. 266, 14703-14708, 1991
A;Title: Granzyme A binding to target cell proteins. Granzyme A binds to and cleaves nucl A;Reference number: A40769; MUID:91317840; PMID:1860869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 68, 73-84, 1988
A;Title: Sequence and structure of the nucleolin promoter in rodents: Characterization of
A;Reference number: 148118; MUID:89121496; PMID:2906027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 6/3; 45/3; 211/1; 273/1; 302/1; 349/2; 391/1; 432/3; 484/1; 525/2; 566/1; 608/
C; Superfamily: nucleolin; ribonucleoprotein repeat homology
C; Keywords: DNA binding; duplication; nucleus; phosphoprotein; RNA binding; transcriptior
P; 310-375/Domain: ribonucleoprotein repeat homology <RRM1>
F; 311-316/Region: RNA-binding RNP2 motif
F; 349-356/Region: RNA-binding RNP1 motif
F; 396-458/Domain: ribonucleoprotein repeat homology <RRM2>
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A;Residues: 2-19;558-567 <YAN>
A;Cross-references: UNIPARC:UPI00001739D0; UNIPARC:UPI00001739D1
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A; Residues: 1-707 <BOU>
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RESULT 1
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                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 23-Jul-1999
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 23-Jul-1999
R;Bourbon, H.M.; Amalric, F.
Gene 88, 187-196, 1990
A;Titles Nucleolin gene organization in rodents: highly conserved sequences within three A;Reference number: JH0148; MUID:90269607; PMID:2347493
A;Accession: JH0148
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A;Cross-references: UNIPARC:UPI0000170A72; GB:M22090; NID:g205793; PIDN:AAA41733.1; PID:
C;Comment: This protein is the major nucleolar-specific protein in eukaryotic exponentia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 68, 73-84, 1988
A;Title: Sequence and structure of the nucleolin promoter in rodents: Characterization A;Title: Sequence and structure of the nucleolin promoter in rodents: Characterization A;Ascession: I63130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-712 <BOUS
A; Cross-references: UPLPARC:UPI000017723A
A; Cross-references: UNDARC:UPI000017723A
A; Note: the authors translated the initiation codon GTG for residue 1 as Val
R; Lischwe, M.A.; Cook, R.G.; Ahn, Y.S.; Yeoman, L.C.; Busch, H.
Biochemistry 24, 6025-6028, 1985
A; Title: Clustering of glycine and Ng, Ng-dimethylarginine in nucleolar protein C23.
A; Reference number: A24088; MUID:86104094; PMID:4084504
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195 DEDEDDEEDDD----EREEDDSEREVWEITTAKGKKTPAKVVPMKAKSVAEEEDDEEEDE 250
                                                                                                                                                                                                                                                                                                                              197 LSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIH 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----AAQAKALVPTPGKKGAATPAKGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 SSSLSASTSVSDSSQKKEEHNYSLFVSDN------LGEQPTKCSP----EEDEED 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----BEEEEDYEDDK 396
                                                                                                                                                                                                                              137 PTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSSKTLQAEVP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                    257 IDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLP-QEGPGSLAAGE 315
                                                                                                                                                                                                                                                                         21 PKEVBEDSEDEEMSEDE----DDSSGEEEVVIPOK-KGKKATTTPAKKVVVSQTKKAAVP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 DDDISDTFSEPGYENDSVEDLKEVTSISSRKRGK------RRYFWEYSEQLTP 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 TP--AKKAAVTPGK--------KAVATPAKKNITPAK-----
                                                                                                                     Query Match
8.0%; Score 188.5; DB 1; Length 707;
Best Local Similarity 23.5%; Pred. No. 0.002;
Matches 84; Conservative 40; Mismatches 113; Indels 121; Gaps
F;524-531/Region: RNA-binding RNP1 motif
F;570-634/Domain: Tibonucleoprotein repeat homology <RRM4>
F;571-576/Region: RNA-binding RNP2 motif
F;607-614/Region: RNA-binding RNP1 motif
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A;Molecule type: DNA
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A;Residues: 651-703 <LIS>
A;Cross-references: UNIPARC:UP1000017723B
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A;Gene: CESP:C34D4.14
A;Map position: 4
A;Introns: 120/1; 201/3; 365/3; 445/2; 509/1; 728/3; 856/3; 902/3; 940/3; 1027/3; 1508/3;
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A;Residues: 1-2761 <DUZ>
A;Cross-references: UNIPROT:Q18447; UNIPARC:UPI000007762A; EMBL:U58755; PIDN:AAB00699.1;
A;Experimental source: strain Bristol N2; clone C34D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1668 NRH---------KOHNKPAASALSRFASVKNTTPAGTPSSGGSSGGAIGKKSM 1711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 EDYEDDKDDDISDTFSE-----PGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 EDEEDEEDDEDEBEEEEFVKAAPGKRKKEMTKQKEAPEAKKQK------IEGSEPTT 308
                                                                                                                                                                                                                                                                                                              129 DEKVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GFGSEHELSENEEEEEE 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C34D4.14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 KILDAEVPLSDCVQKASKPPSSTQIMVKINMYHNEKVNFHVECKDYVKKAKVKINPVQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : :: : | | : | | | : | | ESKKMAPPPKEVEDSEDEEMSEDE----DDSSGEEEVVIPQK-KGKKATTTPAKKVVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGP
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7.6%; Score 178.5; DB 2; Length 2761;
Best Local Similarity 21.6%; Pred. No. 0.039;
Matches 84; Conservative 53; Mismatches 116; Indels 135;
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F;311-376/Domain: ribonucleoprotein repeat homology «RRM1» R;397-459/Domain: ribonucleoprotein repeat homology «RRM2» F;489-552/Domain: ribonucleoprotein repeat homology «RRM3» F;575-639/Domain: ribonucleoprotein repeat homology «RRM3»
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R;Du, Z.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C34D4, A;Reference number: Z20600
A;Reference number: T29285
A;Status: preliminary; translated from GB/EMBL/DDBJ
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R,Jordan, P.; Heid, H.; Kinzel, V.; Kuebler, D.
Biochemistry 33, 14696-14706, 1994
A,Title: Major cell surface-located protein substrates of an ecto-protein kinase are hom
A,Reference number: A55996; MUID:95086063; PMID:7993898
                                                                                                                                   UNIPARC:UPI0000161B7E; GB:M60858; GB:J05584; NID:g185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 231-236;349-362;399-403;458-461;655-656,'X',658-660 <JOR>
A;Cross-references: UNIPARC:UP1000017723C; UNIPARC:UP1000017723D; UNIPARC:UP1000017723E;
A;Experimental source: surface-labelled HeLa cells
                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-707 -68R2-
A; Cross-references: UNIPARC: UP10000161B7E
A; Cross-references: UNIPARC: UP10000161B7E
Mol. Cell. Biol. 13, 4301-4310, 1993
A; Title: Nuclear proteins that bind the pre-mRNA 3' splice site sequence r(UUAG/G)
A; Reference number: A48138; MUID: 93309464; PMID: 8321232
            A;Title: Genomic organization and chromosomal localization of the human nucleolin A;Reference number: A35804; MUID:90368666; PMID:2394707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 KN---GKNAKKEDSDEEEDDDSEEDEBEDEDEDEDEDETEPAAMKAAAAAPASEDEDDED 191
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tive 52; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: DNA binding; nucleolus; nucleus; phosphoprotein; F;308-373/Domain: ribonucleoprotein repeat homology «RRM1> F;394-456/Domain: ribonucleoprotein repeat homology «RRM2> F;487-556/Domain: ribonucleoprotein repeat homology «RRM3> F;573-634/Domain: ribonucleoprotein repeat homology «RRM4>
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                                                                                                                                                                                                        A;Title: Cloning and sequencing of the human nucleolin cDNA. A;Reference number: S04631; MUID:89290043; PMID:2737305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: sequence extracted from NCBI backbone (NCBIP:134645)
                                                                                                          A;Reddues: 1-707 <SRI>
A;Rcoss-references: UNIPROT:P19338; UNIPARC:UPI0000161B7E; (R;Srivastava, M.; Fleming, P.J.; Pollard, H.B.; Burns, A.L. FEBS Lett. 250, 99-105, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 2q12-2qter
C;Superfamily: nucleolin; ribonucleoprotein repeat homology
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                                                                                                                                                                                                                                                                                A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 458-474 <ISA:
A; Cross-references: UNIPARC: UP10000073927
A; Experimental source: HeLa cell nuclei
Biol. Chem. 265, 14922-14931, 1990
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                                                                                           A, Molecule type: DNA
                                                                                                                                                                                                                                                            A; Accession: S04631
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                                                                A; Accession: A35804
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Best Local S:
Matches 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-678 <TRI>
A;Cross-references: UNIPROT:P13816; UNIPARC:UP1000012B0E0; GB:J03998; NID:g160298; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A54514
R;Triglia, T.; Stahl, H.D.; Crewther, P.E.; Silva, A.; Anders, R.F.; Kemp, D.J.
Mol. Biochem. Parasitol. 31, 199-202, 1988
A;Title: Structure of a Plasmodium falciparum gene that encodes a glutamic acid-rich A;Reference number: A54514; MUID:89040048; PMID:2903445
                                                                                                                                                                     é
                                                                               1883 DEEDDDDDDDDDDSSNENQEKLVELLGGERGLFDKLKEVITGESLSDASSSAKDATINEAQ 1942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510
1712 STINLVDERQKTSGPSVASTGQAASAESLQ-HQTPSL----ENLLARAMPHAFGRIAEN 1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glutamic acid-rich protein precursor - malaria parasite (Plasmodium falciparum)
N;Alternate names: GARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKKITSRAAAPVCSSKTLQAEV-PLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVE-- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------CKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398
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                                                                                                                                            ------EDEEDVDDED---HDEGFGSEHELSENEEEEEEE 390
                                                                                                                                                                                                                                        ----TSISS 425
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Date: 23-Oct-1990 #text_change 09-Jul-2004

Accession: 31-5043; S04631; Rel138; A55996

Stivastava, M.; McBride, O.W.; Fleming, P.J.; Pollard, H.B.; Burns, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511 LIGTIGRVNVVPRRDNHKKKMAKIBEAE----LQKQKHVDKEED------KKEESKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVEIINLEDKEACEEQHITVESRPLSQPQCKLIDEPEQLTLMDKSKV---EEKNLSIQEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFVSDNLGEQPTKCSPEEDEEDKEDVDDEDHDEGFGSEHELSENEEEEEEEDYEDDKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQE------BSKEVQE------DEEEVBEDEBEBEBEBEBE--
                                                 ---TSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N,Alternate names: GARP
C,Species: Plasmodium falciparum
C,Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.0%; Score 165; DB 2; Length 67
22.3%; Pred. No. 0.041;
cive 44; Mismatches 101; Indels
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                                                                                                                                                                                                                                          -GYENDSVEDLKEV
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                                                                                                                                                                                                                                                                                                                                                                 426 RKRGKRRYFW-----EYSEQLTPSQQER 448
                                                                                                                                                                                                                                             DYEDDKDDDISDTFSEP-----
                                                   305 QEGPGSLAAGESSSLSAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                               355 EEDE-----
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Superfamily: histone H1
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Best Local 3
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Gaps

-----LQAEVPLS 198

A; Map position: 2L

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A;Residuss: 1-1974 <CON>
A;Cross-references: UNIPROT:Q09612; UNIPARC:UPI000008390B; EMBL:U23452; NID:g733564; PID:
A;Experimental source: strain Bristol N2
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A;Gene: CBSP:R07G3.3
A;Introns: 91/3; 158/3; 244/3; 480/3; 574/3; 722/2; 759/3; 913/2; 948/2; 1114/3; 1323/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1437 ------PDQTTGLK 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1475 TSQQPPSFAAKRPSFGRQAQSSSNVIPPAPAPTPTSQQKVSPVKRPIPPSIPNEPLDIIP 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 NPRDNFLSLEDCKDIENLE-----SFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---STQI---MVKTNMY-----HNEKVNFHVECKD-YVKKAKVKINPVQQSRPLLSQI 255
                                                                                                                                                                                                                                                                                                     142 LN-----SEDSQSVSDSLY-----YP----DSL-----FSVK--QNPLPSSF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 CDIWGTKEVDYLGLDDFSSPYQDEEVISKTPT--LAQLNSEDSQSVSDSLYYPDSLFSVK 164
                                                                                                                                                                                                                                                                                                                                                                        534 LDDFNYIIKIDSWNRIENIYKTWSSKNYPRVKYDKLLWEPIILGPSFGINGMMNLEPTAL 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 AAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFK-FTQ-ELLLSPLPQEGPGSLAAGES 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KRVLESIH-- 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------DRKGI-----DRSKFSTETHWELCFTIKNSETP----LGNH 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 SSLSASTSVSDSSQKKEEHNY--SLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 SEHELSENEEEEEEEEDYEDDKDDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRR 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein R07G3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                   199 DCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTD
                                                                                                                                                      86 SNWEQWDTY----CEDLTKYTKLTSCDIWGTKEVDYLGLDDFSSPYQDEEVISKTPTLAQ
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Query Match 6.8%; Score 160.5; DB 2; Length 1974; Best Local Similarity 21.6%; Pred. No. 0.27; Matches 104; Conservative 51; Mismatches 152; Indels 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1400 NDQINQLKQENLKLTENIRMAQLQSVSATDVESKPGP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riconall, M. submitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid R07G3.
A;Reference number: Z18562
A;Accession: T16703
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molegule type: DNA
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                                                                                  86; Conservative
       Query Match
Best Local Similarity
Matches 86; Conserv
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N;Alternate names: hypothetical protein YBL0507; hypothetical protein YBL0515
N;Alternate names: hypothetical protein YBL0507; hypothetical protein YBL0515
C;Species Saccharomyces cervisian
C;Date: 16-Dec-1993 #sequence revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: S39835; S45787; S37336
C;Accession: Bakkoury, M.; Vierendeels, F.; Dubois, E.; Messenguy, F.
Yeast 9, 1355-1371, 1993
A;Title: Sequencing and functional analysis of a 32 560 bp segment on the left arm of year sequence number: S39824; MUID:94205266; PMID:8154187
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                                                                                  transcription factor 1, neural - rat

N;Alternate names: neural zinc finger factor-1

S;Species: Rattues norvegicus (Norway rat)

C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004

C;Accession: T46637

C;Accession: T46637

C;Accession: T46637

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A;Cross-references: UNIPARC:UP10000135570; EMBL:Z35814; NID:g536078; PIDN:CAA84873.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: UNIPROT:P70475; UNIPARC:UPI00000E86A7; EMBL:U48809; NID:91511631;
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R;Dubois, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, aubmitted to the Protein Sequence Database, August 1994
A;Reference number: S45782
A;Accession: S45787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1187 <JIA>
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Cross-references: SGD:S0000148; MIPS:YBL052c
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Matches 52; Conserv
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A; Residues: 1-831 <SCH>
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ò		Qy 316 -SSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQP-TKCSPEEDEEDV 364
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ර සි	310 SLAAGESSSLSASTSVSDSSQKKEHNYSLFVSD 343	OY 365 DDEDHDEGFGSEHELSENEREREEEDVEDDKDTSPFG 408
3 8		Db 1082 DEEEDEAQDDDNEENQDDDDDDGDDGSPRPG 1114
S 8		RESULT 10
l á		S38149 S1S2 protein – veast (Saccharomyces cerevisiae)
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C; Speci	es: Arabidopsis thatiana (mouse-ear cress)	A, Experimental source: strain S288C B.di Cmm C.J. Bose, R.: Arndt, K.T.
C;Date: C;Acces	02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 03-301-2004 sion: G86266	Genetics 139, 95-107, 1995
R; Theol	ogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Ching, M.K.; Conn. L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;	
ansen,	N.F.; Hughes B.; Huizar, L.	A.Accession: S54982 A.Molecule type: DNA
Nature A;Autho	408, 815-820, 2000 prs: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.	A.Residues: 1-562 <din> A.Residues: 1-562 <din> A.Residues: 1-562 <din> A.Residues: 1-562 <din> A.Residues: 1-562 <din> A.Residues: 1-562 <din 1-562="" 1-562<="" <din="" a.residues:="" td=""></din></din></din></din></din></din>
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A; Author ker, M.	)rs: Salzberg, S.D.; Schwartz, U.K.; Shinn, F.; Southwick, A.M.; Sun, D.; Traser, C.C., Venter, J.C.; Davis, R.W. Commons and analysis of chromosome I of the plant brabidonsis.	A, Cons. references: SGD:S0001780; MIPS:YKR072c A, Map position: 11R
A) TICIL	ence number: A86141; MUID:21016719; PMID:11130712	C; Keywords: nucleus
A;Accel A;Statu A:Molec	A;Accession: use.co. A;Status: preliminary A:Molecule type: DNA	6.6%; Score 157; DB 2; Length 562; illarity 20.5%; Pred. No. 0.093;
A;Resic	lues: 1-1128 <sto></sto>	Matches 86; Conservative 64; Mismatches 120; indels 150; Gaps 15;
A; Cross		
י קשויי (א	מסדרדמון: ד	Db 174 KIVDIMKPDKIMATSTPISRENNKVTAKAPTSITLRKEDAQDQANNVSGQINVRSTPEET 233
Ouer) Best	Query Match 6.7%; Score 159.5; DB 2; Length 1128; Best Local Similarity 23.3%; Pred. No. 0.16; Matches 108: Conservative 65: Mismatches 176: Indels 115; Gaps 23;	TSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMV
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ò	190TLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVE 230	
QQ	850 GIDTGKPEQRLSSSVAVGMETKGEKPLPVDLRLRPSSSSIPEEDEEYTDSRVQETSEGSQ 909	KKOLOTIKEEMSWUTVPKPSEKVMDINGDIGLGGMMDWNEIVNKIVMKIVGGYPKNNEEBD
ò	231CKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENT 264	357
qq	910 LSEFQSSRRGRGRPRKAKPALNPISSVKHASLEESSKDELSGHVSVTSKKTTGGGGRKRQ 969	200
ò	265CYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGE 315	

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-338,'S',340-500 <BRO>
A;Cross-references: UNIPARC:UPI000012B0DD; EMBL:Z99091; PIDN:CAB11772.1; GSPDB:GN00066; & A;Experimental source: strain 972h-; cosmid c13F5
C;Genetics:
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A;Cross-references: UNIPROT:062348; UNIPARC:UPI00007DBCA; EMBL:Z83122; PIDN:CAB05601.1;
A;Experimental source: clone R11A5
A, Status: nucleic acid sequence not shown; not compared with conceptual translation
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24169
R;MCMurray, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19848
A;Accession: T24169
A;Accession: T24169
A;Accession: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 KASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 NTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 TSVSD-----SSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 KDKTSVKKSVKETAS----KKGAIEKPSKSKKITKEAAKEIAKOSSKT-----DVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 KKSK------KEAKRASSPEPSKKSVKKQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93;
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                                     A;Molecule type: mRNA
A;Residues: 374-407 <VAN>
A;Cross-references: UNIPARC:UPI000017A376
**Sirown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood,
submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 500;
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A;Introns: 14/2; 40/3; 277/3; 308/3; 353/3; 550/1; 658/1; 798/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 1
F;264-331/Domain: ribonucleoprotein repeat homology <RRM1>
F;367-433/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.5%; Score 152.5; DB 2; Best Local Similarity 23.4%; Pred. No. 0.15; Matches 75; Conservative 38; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
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6.5%; Score 152.5; I
Best Local Similarity 32.3%; Pred. No. 0.3;
Matches 43; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGKRRYFWEYSEQLTPSQQER 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: gar2; SPDB:SPAC13F5.09
                                                                                                                                                                                                                     A; Reference number: Z21733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Gene: CESP:R11A5.1b
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CLYI.; Genet. 29, 307-318; 1996
A;Title: Molecular analysis of a novel Schizosaccharomyces pombe gene containing two RNF A;Reference number: S68083; MUID:96171513; PMID:8598051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleolar protein gar2 - fission yeast (Schizosaccharomyces pombe)
NyAlternate names: probable RNA-binding protein RBD18
C.Species: Schizosaccharomyces pombe
C.Species: Schizosaccharomyces pombe
C.Accession: S55785; S60087; T37634; S52318
R;Gulli, M.P.; Girard, J.P.; Zabetakis, D.; Lapeyre, B.; Melese, T.; Caizergues-Ferrer, Nucleic Acids Res. 23, 1912-1918, 195
A.Title: garz is a mucleolar protein from Schizosaccharomyces pombe required for 18S rRN A; Accession: S55785
A.Status: nucleic acid sequence not shown
A; Residues: 1-500 <GULLA.
A; Residues: 1-500 <GULLA.
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A; Residues: 1-500 <GULLA.
A; Residues: 1-50
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A;Experimental source: strain 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |::| || | | ::| || 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 KVGKNSL--NRKYLENL-KDNKRKNNNYSGRNNKYKGDGANDKDKSIDKNESEGGDHSEI 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 HATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDN 344
                                                                                                                                   C;Species: ateline herpesvirus 3
A;Variety: strain 73
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42963
R;Albrecht, J.C.; Fleckenstein, B.
submitted to the RMBL Data Library, August 1998
A;Description: Primary structure of the herpesvirus ateles genome.
A;Reference number: Z22274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 SILGSRGIGLDLFRTQDVLKFPSSDAKFMAVSQPDNFNEKEVEFSMTGGKTDSEDVTAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 WGTKEVDYLGLD--DFSSPYQDEEVISKTPTLAQLNSEDSQSV-SDSLYYPDSLFSVKQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 LGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHELSENEEEEEEEEDYEDDKD-DDISDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : : |: : | | | | | 410 NREKNRKRKKPNGFRVGDKEVGEEKSVKSGEGKK-SEKDSEERAEDKDEERN----KKKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.5%; Score 153; DB 2; Length 79. Best Local Similarity 22.6%; Pred. No. 0.24; Matches 85; Conservative 62; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 PLPSSFPG-KKITSRAAAPVCSSKTLQAEVPLSDCV------
                                                                                                                    hypothetical protein 48 - ateline herpesvirus 3 (strain 73)
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: T42963
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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524 EDEEDEEDEEEEDEE 539
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647 EAWSKKISSSPWWCFA-----KNVSKFDGSDNSILPEGAFRLKNENDQNHLP---PAQ 696
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                                                                                                                                                                                                               254 QIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALP---FKETQELLLSPLPQEGPGS
                                                                                                                                                                                                                                                                                                                                                                                         311 LAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHD
                                                                        Query Match 6.4%; Score 152; DB 2; Length 1038; Best Local Similarity 24.8%; Pred. No. 0.38; Matches 61; Conservative 40; Mismatches 89; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 EGFGSEHELSENEEEEEEEDYEDDKDD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: February 28, 2006, 08:54:18 Job time : 28.3216 secs
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A;Cross-references: SGD:S0005930
A;Map position: 16L
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Nolecule type: DNA
Nolecule type: DNA
Nolecule type: DNA
Nolecule type: UNIPROT:012532; UNIPARC:UP10000052E40; EMBL:Z48483; NID:g683777; PID
NECTORAL SOURCE: STRAIN AB972
Note: Strain AB972
Nolection of Strain AB972
Nolection of Strain AB972
Nolection: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
Nolection of Saccharomyces cerevisiae chromosome XVI left arm.
Nolection of Saccharomyces cerevisiae chromosome XVI left arm.
Nolection of Saccharomyces cerevisiae chromosome XVI left arm.
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.Residues: 1-1038 <HAL>
.Cross-references: UNIPARC:UPI0000052E40; EMBL:U33335; NID:g965076; PID:g965084; MIPS:Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Cross-references: UNIPROT:045718; UNIPARC:UPI0000083395; EMBL:283122; PIDN:CAB05598.1;
Experimental source: clone R11A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ypothetical protein YPL009c - yeast (Saccharomyces cerévisiae)
1/Alternate names: hypothetical protein LPA8c; hypothetical protein YP8132.04c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 QELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 EDEEDEEDVDDEDHDEGFGSEHELSENEEEEEEEDVEDDKDDDISDTFSEPGYENDSVE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 EDEEDBEDVDDEDHDEGFGSEHELSENEEEEEEDYEDDKDDISDTFSEPGYENDSVE 415
                                                                                                                 Species: Saccharomyces cerevisiae
Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
Accession: S52522; S59684
                                                                                                                                                                                                                                                                                                                                                                    ypothetical protein R11A5.1a - Caenorhabditis elegans 'Species: Caenorhabditis elegans ; Species: Caenorhabditis elegans ; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004; Accession: T24166 ; Accession: T24166 ubmitted to the EMBL Data Library, November 1996 ; Reference number: Z19848
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Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
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           Q5cvu2
Q54v59
Q7rie9
Q55sc9
Q9c2h4
Q7ryc8
Q7ryc1
Q8i510
Q8ibj8
Q4wpx3
Q4wpx3
Q4wpx3
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05kmz9
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Last sequence update)
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Pred. No. 4e-113;
0; Mismatches 1;
           QSCVU2_CRYPV
QS4V59_DICDI
QYRIEZ_PLAYO
QS5SC9_CRYNE
Q97R51_NEUCR
Q97R51_NEUCR
Q81BJ0_PLARY
Q4WFX3_ASPFU
Q4WFX3_ASPFU
Q4WFX3_ASPEU
Q95XW6_CREEL
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01-MAR-2003 (TrEMBLrel. 23, L
01-MAR-2004 (TrEMBLrel. 26, L
Adult retina protein.
Homo sapiens (Human).
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OBIZGI;
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  1018
1308
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300

360 360 420

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NCBI_TaxID=9606;
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A Itschul S.F., Zeeberg B., Buetow K.H., Schefer C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.R., Shalar N.K.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

A Brapleton M., Soarse M.B., Bonaldo M.F., Carainor P.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Torshiyuki S., Carainor P.L., Frange C.,

A Brownstein M.J., Usdin T.B., Torshiyuki S., Carainor P., Prange C.,

A Brownstein M.J., Widnam P.J., McKernan K.J., Marake J.H., Gunzarene P.H.,

A Broak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunzarene P.H.,

Rhialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabe J., Helton B., Ketteman M., Madan A., Rodriques S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Schmutz J., Myers R.M.,

Rodriguez A.C., Girmwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Girmwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                       Name-LOC153222;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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TISSUE-Lung;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041709; AAH47709.1; -; mRNA.
Ensembl; ENSG0000164463; Homo sapiens.
InterPro; IPR004827; TF bZIP.
PROSITE; PS00036; BZIP BASIC; UNKNOWN 1.
SEQUENCE 639 AA; 72118 MW; ECFB92D9290DEDEB CRC64;
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                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                   639 AA
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                421 TSISSRKRGKRRYFWEYSEQLTPSQQER 448
TSISSRKRGKRRYFWEYSEQLTPSQQER
                                                                                                                               Created)
                                                                                                                             01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                               QBIURG HUMAN PRELIMINARY,
QBIURG;
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Matches 447; Conservative
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Director MGC Project;
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                            301 SPLPOEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEED
                                                                                                                                                                                                             361 EEDVDDEDHDEGFGSEHELSENEEEEEEEEDYEDDKODDISDTFSEPGYENDSVEDLKEV
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The German CDNA Consortium;
The German CDNA Consortium;
Kochrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger Robo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX647573; Ca146.04.1; -; mRNA.
InterPro; IPR004827; TF bZIP.
PROSITE; PS06036; BZIP_BASIC; UNKNOWN I.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein DKFZp313F2319 (Fragment).
Mame=DKFZp513F2319 (Fragment).
Homo sapiens (Luman).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 604 AA.
                                                                                                                                                                                                                                                                                                                                 TSISSRKRGKRRYFWEYSEQLTPSQQER 448
                                                                                                                                                                                                                                                                                                  TSISSRKRGKRRYFWEYSEQLTPSQQER
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QSHYKO;
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NON TER 604 61
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Genome Res. 10:1617-1630(2000).
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                                               EEDVDDEDHDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/67; TISSUE=restis; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hayashizaki Y.; Hiquency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                       01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis CDNA, RIKEN full-length enriched
library, clone:4932441F15 product:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                     640 AA.
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                                                                                                                                         TSISSRKRGKRRYFWEYSEOLTPSOOER 448
                                                                                                   TSISSRKRGKRRYFWEYSEQLTPSQQER
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                                                                                                                                                                                                                                     QBCDGS_MOUSE PRELIMINARY;
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the RIKEN Genome Explo
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                                                                                                                                                                                                                                                                                                                                                                                               Name=A930001N09Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL 120
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Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Futuda S., Puruno M., Hanagaki T., Hara A., Hashizume W., Hayatsu M., Hiramoto K., Hiraoka T., Hirozane T., Hayatsu M., Hiramoto K., Konno H., Konno H., Konno H., Konno H., Konno H., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saito H., Sakai C., Sakazume N., Sano H., Asaski D., Shibata K., Shinagawa A., Takada C., Sakazume N., Sano H., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Yagari C., Yakanishi A., Muramatsu M., Hayashizaki Y.; Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AK030092; BAC26779:1; -; MRN.
EMBL; AK030092; BAC26779:1; -; MRN.
EMBL; AK030092; BAC26779:1; -; MRN.
EMBL; MGI:1924378; A930001N09Rik.

RITHEFPC: IPRO04827; FF DZIP.

PROSTITE: PSO0036; BZIP_BASIC; UNKNOWN_I.
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STRAIN=CSBL/GJ; TISSUE=Testis;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Komon H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumino. F., Matsuncto H., Saksguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rawi T., Rayashizaki Y.; Rawi T., Bequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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Matches 415; Conservative
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NCBI_TaxID=9606;
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Matches 407;
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EMBL, EX647768; CAI46039.1; -; mRNA.

Hypothetical protein.

NON TER 408 408
                                                                                    Q5HYG4 HUMAN PRELIMINARY; PRT; 408 AA.
Q5HYG4;
10-MAY-2005 (TEMBLrel. 30, Last sequence update)
10-MAY-2005 (TEMBLrel. 30, Last annotation update)
10-MAY-2005 (TEMBLrel. 30, Last annotation update)
10-MAY-2005 (TEMBLrel. 30, Last annotation update)
Hypothetical protein DKFZp686G2059 (Fragment).
Name-DKFZp686G2059;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordatap; Primates; Catarrhini; Hominidae;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Cz
01-JUN-2003 (TrEMBLrel. 24, La
01-JUN-2003 (TrEMBLrel. 24, La
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                              The German cDNA Consortium;
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                                                                                                                                                                                                                                                                                                                          Homo.
NCBI_TaxID=9606;
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Mus musculus (Mouse)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Murcidea; Muridee; Musinee; Mus.
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MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A93,0040G19 product:hypothetical protein, full insert sequence.
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
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                                                                                                                                                                              Length 417;
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                     Li F., Yao K.T.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX174896; AAO18732.1; -; mRNA.
Hypothetical protein.
SEQUENCE 417 AA; 46579 MW; 9DBD37B07C14556B CRC64;
                                                                                                                                                                            90.9%; Score 2148; DB 2;
99.8%; Pred. No. 1.2e-102;
iive 0; Mismatches 1;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kutels S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P., Roustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whinhaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hasebi V., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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STRAIN=C57BL/G1 TISSUE-Retina;
STRAIN=C57BL/G1 TISSUE-Retina;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunioto H., Sakaguchi S., Ikegami T., Kashinaji K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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The FANTOM Consortium,
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SEQUENCE 351 AA; 3
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                                1 MPQPSVSGMDPPFFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                       61 SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL
1 MPQPSVSGMDPPFGDAFRSHIFSEQTLMSTDLLANSSDPDFWYBLDREMNYQQNPRDNFL
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01-0TN-2001 (TrEMBLrel. 17, Last sequence update)
01-0TN-2001 (TrEMBLrel. 17, Last annotation update)
01-0TN-2001 (TrEMBLrel. 17, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930001N09 product:hypothetical protein, full insert sequence.
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Q9CTQ7;
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DB 2; Length 351;

Score 1704.5; DB 2; Length Pred. No. 5.9e-80; 9; Mismatches 16; Indels

72.1%; ilarity 92.6%; Conservative

Best Local Similarity Matches 325; Conserv

Query Match

351 AA; 39254 MW; ABA4B36D996AFAAD CRC64;

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61 SMEDCKDLENLESFTDILDKEAAFTSKWEQWDTYCEDLIKYTKLTSCDIWGTKEVDYLGL 120
241 VKINPVQQGRPLLSQVHIDAAKENTCYCGAVAKRQERRGVEPHQGRGTPALPFKETQELL 300
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Tetradon nigroviridis (Green puffer).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Meopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CB; TISSUE-Bursa;
caddwell R.B., Katezek A.M., Arakawa H., Bezzubov Y., Zaim J.,
Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
Full-length cDNAs from chicken bursal lymphocytes to facilitate
genefunction analysis.";
Genome Biol. 6:R6-R6(2005).
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical J. A.M. Hypothetical A.M. A.D. 15183 MW; AD73D84C28DE3670 CRC64;
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90.1%; Pred. No. 1.3e-26;
live 6; Mismatches 7; Indels
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 7 SCAF15001, whole genome shotgun sequence.
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Last annotation update)
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Q4RRX3;
                                                                                                                                                                                                                                                                   CHICK PRELIMINARY;
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25-OCT-2004 (TrEMBLrel.
Hypothetical protein.
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Q4RRX3_TET
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A Arakawa T., Arai A., Aono H.,
A Arakawa T., Azawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramcto K., Hiracka T., Hori F.,
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A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Okazaki Y., Okido T., Owa C., Saito H., Saito H., Sakai C., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamaura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (AUG-2000) to the EMBL/GanBank/DDBJ databases.
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                                             The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUB=Retina; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibate K., Titoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibate K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sunbate M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sunn N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumura S., Ikeguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Tawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Nkriki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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Ensembl; ENSMUSG00000048249; Mus musculus.
MGI; MGI:1924378; A930001N09Rik.
Hypothetical protein.
                                   STRAIN-C57BL/6J; TISSUE=Retina;
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Matches 306; Conservative
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                                   NCBI_TaxID=37296;
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Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Jubin C., Castelli V., Poulain J., De Berardinis V., Cruaud C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lindblad-Toh K., Barten B., Nusbaum C., Kahn D., Robinson-Rechavi M., Hauder P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                          217 TRPVPSSTETMAKNQ-----NLFSLSQDYGQGQPKLQARATKWAAP--APHNSDFVPP
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34.0%; Pred. No. 3.2e-25;
tive 56; Mismatches 104; Indels 162; Gaps
                                                                                                                                                                                                                      CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
Genoscope, Whitehead Institute Centre for Genome Research,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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600 AA; 66291 MW; B2F28B2F3B27B1C4 CRC64;
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Last annotation update)
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                                                                                                                                     the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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Matches 166; Conservative
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Q9DUNO;
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Orf73.
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Q9DUNO HHV8
ID Q9DUNO;
AC Q9DUNO;
DT 01-MAR-;
DT 01-MAR-;
DT 01-MAR-;
DE Orf73.
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MEDLINE=20381179; PubMed=10900044;

MEDLINE=20381179; PubMed=10900044;

MEDLINE=20381179; PubMed=10900044;

MEDLINE=20381179; PubMed=10900044;

"Hot-spot variations of Kaponi's sercoma-associated herpesvirus latent nuclear antigen and application in genotyping by PCR-RFLP.";

"Hot-spot variations of Kaponi's sercoma-associated herpesvirus latent nuclear antigen and application in genotyping by PCR-RFLP.";

J. Gen. Virol. 81:2049-2058(2000).

EMBL; AAP192756; AAG0155.1; -1.

GO; GO:0005885; C:cytoskeleton; IEA.

InterPro; IPR002017; Spectrin.

SEQUENCE 976 AA; 112017 MW; ES781EZA509FF70B CRC64;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
NCBI_TaxID=37296;
[1]
Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                MEDLINE=99445611; PubMed=10515805; DOI=10.1086/315098; Gao S.J., Zhang Y.J., Deng J.H., Rabkin C.S., Flore O., Jenson H.B.; Moolecular polymorphism of Kaposi's asrcoma-associated herpesvirus (Human herpesvirus 8) latent nuclear antigen: evidence for a large repertoire of viral genotypes and dual infection with different viral
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24.0%; Pred. No. 0.074;
tive 56; Mismatches 149; Indels 7
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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Q91LX9;
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991LX9 H1V9

1091LX9 H1V9

AC 091LX9 F

DT 01-DEC-C

DT 01-MAR-2

DT 01-MAR-2

DE ORP73

OC VITUBESS

OC Gammahes

OC Gammahes
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InterPro; IPR002017;
SEQUENCE 1129 AA;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
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                                                                                                                                                                                                                                                                                                                                                                          89;
                           MEDLINE=21376412; PubMed=11483733; DOI=10.1128/JVI.75.17.7882-7892.2001; Garber A.C., Shu M.A., Hu J., Renne R.; Phinding and medulation of gene expression by the latency-associated nuclear antigen of Kaposi's sarcoma-associated
                                                                                                                                                                                                                                                                                                                          Length 1003;
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                                                                                                                                                                            J. Virol. 75:7882-7892(zuu1).

EMBL; AR360120; AAK50002.1; -; Genomic_DNA.
GO; GO:0005856; C:Cytoskeleton; IEA.
InterPro; IPR002017; Spectrin.
SEQUENCE 1003 AA; 115517 MW; C20C43308B01A0A3 CRC64;
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Last annotation update)
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                                                                                                                                                          herpesvirus.";
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                                                                                                                                                                                                                                                                                                                                                                   SSPYODEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA
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                                                                                                                                                   Length 1129;
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MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
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SEQUENCE 2649 AA; 309810 MW; E7207F344643AC24 CRC64;
                                                 8F63855B45F79109 CRC64;
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Nature 413:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                        DB 2;
                                                                                                                                                        8.1%; Score 191.5; DB 2;
25.0%; Pred. No. 0.12;
ive 52; Mismatches 142;
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EMBL; AABLO1002172; EAA18637.1;
InterPro; IPR011591; Botulinum.
ProDom; PD001963; Botulinum; 2.
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Q7RAS7;
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                                                                                                                                                                                                                                                                      93; Conservative
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Name=PY06422;
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Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996)

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                                                                                                                                                                                                                                                                                                                                                                              328 YN------AGLKNEKIENIR----KIGNKSKGKNTILKKIGVHWENKKEMQNEESY- 373
                                                                                                                                            51 YQQNPRD----NFLSLEDCKDIENLESFIDVLDNEGALISNWEQWDTYCEDLIKYTKLTS 106
                                                                                                                                                                                                                107 CDIWGTKEVDYLGLDDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQN 166
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Cesarman E., Nador R.G., Bai F., Bohenzky R.A., Russo J.J.,
Moore P.S., Chang Y., Knowles D.M.;
"Kaposi's sarcoma-associated herpesvirus contains G protein-coupled
receptor and cyclin D homologs which are expressed in Kaposi's sarcoma
                                                                                                                                                                  200 LKKNNFDDATKHFMKPKTFKDINGLYYDT----NEKAIDIDLLKMEH--EKLTRMSSLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
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                                                                      15 DAFRSHTFSE-----QTLMSTDLLANSSDPDFMY------ELDREM-----N
                                                                                            167 PLPSSFPGKKITSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVN
                                                                                                                                                                                                                                                                                                                                                          227 FHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHA
                                                                                                                                                                                                                                                                                                                                                                                                                                287 TPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLG
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                                      Gaps
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                                      169;
   Length 2649;
                                    Indels
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
ORF 73.
Query Match 8.1%; Score 190.5; DB 2; Best Local Similarity 20.6%; Pred. No. 0.36; Matches 93; Conservative 74; Mismatches 116;
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-----DEEEEEEEVESYKKHTYKSGKRR 456
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J. Virol. 70:8218-8223(1996).
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Q98148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 ATPALPP--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 AKVKINPVQQSRPLL----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH
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8.0%; Score 190; DB 2; Length 1162;
Best Local Similarity 24.2%; Pred. No. 0.15;
Matches 94; Conservative 50; Mismatches 137; Indels 108; Gaps
                                                                                                                             Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, U52064, AAC55944.1; -; Genomic_DNA.

EMBL, U75698, AAC57158.1; -; Genomic_DNA.

EMBL, U76698, AAC57158.1; -; Genomic_DNA.

EMPL, U76698, AAC57158.1; -; Genomic_DNA.

SEQUENCE 1162 AA, 135213 MW; 1A72CE01C1CB0B1C CRC64;
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5.1.7 Biocceleration Ltd.	h time 0.685046 Seconds alignments) Million cell updates/sec				2443163						y chance to have a he result being printed, distribution.		Description	Aaws6247 Anti-infl Abg77780 Targettin	Aaps162/ Motif use Aar41636 Internali Aar54662 Native se		Aaw77469 Tetrapept Aaw37726 Cytochrom	Aaw46523 Peptide c Aaw87483 HIV-1 MO/ Aaw87477 HIV-1 mut	Aay21283 Human sem Aaw55768 Immunisat	Aaw47950 AE101 ana Aay85398 IL-2 deri	11-2 11-2	Aab14508 Sterile a Aay99633 Insectici	Aab86380 Cathepsin Aab73471 Mammallan Aau99275 Synthetic
GenCore version 5.1.7 Copyright (c) 1993 - 2006 Bioccel	on: February 28, 2006, 08:37:25, Searc (without 1282.772	Title: US-10-717-665A-44_COPY_448_449 Perfect score: 10 Sequence: 1 RM 2	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 2443163 segs, 439378781 residues	Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	ایم	<ol> <li>geneseqpzuuus:</li> <li>geneseqpzuus:</li> <li>geneseqpzuus:</li> </ol>		Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score d	SUMMARIES	* Result Query No. Score Match Length DB ID	10 100.0 3	10 100.0 4 1 10 100.0 4 2 10 100.0 4 2	10 100.0 4 2 10 100.0 4 2	10 100.0 4 2	001 01 00	10 100.0 4 2	10 100.0 4	10 100.0 4 3 10 100.0 4 3	10 100.0 4 3 AAB1450 1 10 100.0 4 3 AAY9963	447

Aau73263 Human pro Abb84331 Human MBP Abj26706 Seed deve Abb99613 Peptide d		Ado38266 Modified Ado38670 Melanocyt Ado39060 Ebola vir Ady86552 Human VEG		Aar71657 Natriuret Aar54661 Native se Aaw02183 Residues Aaw04336 ATP dipho
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## ALIGNMENTS

AAW56171-248 represent anti-inflammatory tripeptides of the invention.

They are derived from the formulae: Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-CC They are derived from the formulae: Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-CC Glu, or Glu-arg-Xaa, where Xaa = any amino acid residue. Cyclic cdrivatives of the peptides also function as anti-inflammatory agents.

CC The peptides can be covalently linked to one another either directly or CC through a spacer. The peptides and their derivatives have macrophage inhibitory and T-cell inhibitory activity and thus, anti-inflammatory cc activity. The peptides and compositions have anti-immune activity, i.e. cinhibitory effects against a cellular and humoral immune response, es and derivatives - used for treating, e.g. litis, auto-immune disease, allergy asthma, ansplant rejection or Alzheimer's disease. phage inhibitory activity; fibronectin; ty; adherence; extracellular matrix; tor expression; inflammation. serman P, Hirschberg DL; le; 3 AA. English. O LTD. tide. 376P. 3141. 4301. 0295.  $\overline{z}$ 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes an isolated peptide of 100 amino acids or less in size. The peptide is useful for treating a disease state, e.g. cancer, arthritis, diabetes, inflammatory disease, atherosclerossis, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease. This sequence represents a human targeting peptide selective for human organs, tissues or cell types
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including a response not associated with inflammation. The peptides also inhibit the ability of macrophages and T-cells to adhere to extracellular matrix components and fibronectin, as well as up-regulated fas receptor expression in T-cells. They can be used to inhibit unwanted immune
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                                                                                                                                                                                                                                                                                                                                                                                                                  Targetting peptide selective for human organ, tissue or cell type #313.
                                                                                                                                                                   Gaps
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                                                                                                                                   100.0%; Score 10; DB 2; Length 3; 100.0%; Pred. No. 2e+06;
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                                                                                                                                                                                                                                                                                                                      ABG77780 standard; peptide; 3 AA
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Best Local Similarity 100.
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                                                                     reaction and inflammation
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Sequences will normally be part of 9-15 amino acid sequence, excluded as motifs for immunisation but useful in tolerisation. . (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                     based on the amino acid sequence the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Internalisation signal, core, modulation, receptor, transport, ligand, cytoplasmic tail, endocytosis.
                                                                                        Motif useful in tolerization alone or in association with epitopes to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                           Autoantigen; MBP; myelin basic protein; transplantation antigen;
myasthenia gravis; myasthenics; Transplantation antigen.
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                                                                                                                                                                                                                                                                                                                                                        Oligopeptide and polypeptide compsns. - of an immunogen and used for modulating
                                                                                                                                                                                                                                                                                 (STRD ) UNIV LELAND STANFORD JUNIOR.
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            AAP91627 standard; protein; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page; 7pp; English.
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                                                                                                         proteolipid protein.
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                                   AAP91627;
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An antigenic conjugate, useful as a vaccine for AIDS, has the formula (SPNE). (OMPC), where SPNE is a selected principal neutralisation epitope of HIV, which is one of 16 specified polypeptides (including the present sequence) or their fragments containing at least 5 amino acids; OMPC is purified outer membrane proteosome of Neisseria (pref. N. meninglitidis); and n is 1-200, indicating the number of SPNE moieties covalently linked to the OMPC. The conjugates may be substituted by anions, and conjugation may be via a bigeneric spacer. The SPNE polypeptides bind an HIV broadly neutralising monoclonal antibody (559 antibody) that binds gpl20 and also inhibits the binding of HIV to CD4. They were originally identified in the bitope polypeptides accessible to the antibody. The libraries were ALPHA and EPSILON described in AAR83295 and AAR83299 respectively. The sequences of these polypeptides were deduced from their corresponding DNA sequence.
                                    This sequence corresponds to AA 330-333 of amyloid precursor protein. This peptide, which partially overlaps the C-terminal side of thet actisequence RERMS (AARS4661), acts to antagonize the activity of secreted APP (695 AA). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antigenic conjugate useful as vaccine for AIDS - comprising HIV principal neutralisation epitope covalently linked to outer membrane proteosome of Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     selected principal neutralisation epitope; vaccine; HIV; membrane proteosome; Neisseria; OMPC; AIDS; 559 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV principal neutralisation epitope binding to 559 antibody.
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Claim 52; Page 11; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR93665 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                 Modulating receptor mediated transport of ligand into cell introducing heterologous internalisation signal into cell.
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                                                                                                         (SALK ) SALK INST BIOLOGICAL STUDIES (SCRI ) SCRIPPS RES INST.
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Synthetic

AAR54662;

AAR54662

Query Match Best Loca Matches

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Saitoh T;

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AAW77469 standard; peptide; 4 AA.
                                                                                                                                                                                                          Key
Modified-site
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                                                                                                                                                                                                                                                                                        EP725075-A1.
                                                                                      06-JUL-1999
                                                                                                                                                                                   Synthetic.
                                                                 AAW77469;
                                                                                                                                                                                                                                                                                                                                                                                                        Dive V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                    RESULT 8
AAW77469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is a specific example of new peptide derivatives containing the sequence -Phe-psi[PO2CH2]-X-Y-Z'- in which Y = Arg or Lys; X and Z'= natural or pseudo-amino acids (preferably X is Gly, Ala or Leu and Z' is Met, Nle, Ala or Phe!; and -psi[PO2CH2] indicates replacement of the peptide linkage -CONH- between Phe and X by the group -PO2CH2. These peptides are inhibitors of the zinc-dependent endopeptidase EC.3.4.24-15 and so prevent degradation of e.g. somatostatin, bradykinin, angiotensin, neurotensin, substance P, dynorphin etc. and may prevent maturation of ras oncoprotein. They are useful in treatment of pain, hypothermia, arterial hypothermia, cancer and Alzhaimer's disease. They are very selective for 24-15 with no significant action on other zinc endopeptidases such as 24-16, and are more stable, chemically, than phosphonamide peptide derivatives
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/note= "Z-Phe-psi[PO2CH2]-Ala, where Z is benzyloxy-carbonyl and -psi[PO2CH2]- indicates replacement of the peptided linkage -CONH- between Phe and Ala by the group PO2CH2-"
                                                                                                                                                                                              Zinc endopeptidase; EC.3.4.24-15; selective inhibitor; analgesic; pain; hypothermia; arterial hypertension; cancer; Alzheimer's disease; phosphinic acid; pseudopeptide linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide derivs. contg. phosphonic acid gp. replacing an amide bond are highly specific inhibitors of endo:peptidase 24-15, for treating hypothermia, hypertension, cancer, Alzheimer's disease etc.
 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 10; DB 2; Length 4; 100.0%; Pred. No. 2e+06; cive 0; Mismatches 0; Indels
                                                                                                                                                                        retrapeptide useful as zinc endopeptidase 24-15 inhibitor.
 0; Indels
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 12; 18pp; French.
                                                                                                        AAW86792 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yiotakis A;
                                                                                                                                                                                                                                                                                                                                                                                                    96EP-00400229.
                                                                                                                                                      (first entry)
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jiracek J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-356059/36
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Best Local Similarity
Matches 2; Conserv
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Modified-site
                         1 RM 2
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                                                                                                                                                       06-JUL-1999
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                                                                                                                                                                                                                                                   Synthetic
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      Matches
                                                                                   RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                  1...2
/note= "Z-Phe-psi[PO2CH2]-Gly, where Z is benzyloxy-carbonyl and -psi[PO2CH2]- indicates replacement of the pepide inhage -CONH- between Phe and Gly by the group PO2CH2-"
                                                                                                     Zinc endopeptidase; EC.3.4.24-15; selective inhibitor; analgesic; pain; hypothermia; arterial hypertension; cancer; Alzheimer's disease; phosphinic acid; pseudopeptide linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide derivs. contg. phosphonic acid gp. replacing an amide bond are highly specific inhibitors of endo:peptidase 24-15, for treating hypothermia, hypertension, cancer, Alzheimer's disease etc.
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                                                  Tetrapeptide useful as zinc endopeptidase 24-15 inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 13; 18pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96EP-00400229
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-356059/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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ID AAW3
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Gaps

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Conservative

1 RM

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Peptides AAW46520-53 contain protease binding sites. They are used to produce novel reagents whose fluorescence increases in the presence of particular proteases. These fluorogenic protease indicators (substrates) convoided high intensity fluorescent signal at a visible wavelength when they are digested by a protease. The fluorogenic indicators have the contenting a protease binding site, e.g. AAW46520-53. Fl and F2 are contenting a protease binding site, e.g. AAW46520-53. Fl and F2 are contenting a protease binding site, e.g. AAW46520-53. The and F2 are conformation-determining regions that introduce a bend into the composition which positions the fluorophores adjacent to each other with a separation of less than 100 Angstrom. When n is 1, 31 is content the terminal alpha amino group of C1 by a peptide bond. The protease indicators are used for detecting protease of indicators are used for detecting protease activity in a biological sample. The sample is contacted with the indicator and any change in fluorescence is detected, an increase in contacted for detecting protease activity.
                                                                                                                                                                                                                                Fluorogenic substrates for protease determination - having two closely spaced fluorophores flanking protease binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus-1; HIV-1; protease; provirus; L-2 cell; mutation; Nef protein; immunogen; apoptosis; treatment; hybridisation; cell lysis; chemotherapeutic; toxin; HIV infection; MO/LAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 10; DB 2; Length 4; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV-1 MO/LAI env gp120 amino acid fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "encoded by GAA"
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                                                                                                                                                                                                                                                                                                 Disclosure; Col 4; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus 1.
                                                            94US-00331383
                    95US-00549008
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                                                                                                                                             Packard BS, Komoriya A;
                                                                                                    ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                        WPI; 1998-158345/14
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                    27-OCT-1995;
                                                            28-OCT-1994;
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11-FEB-1999
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying DNA encoding inducible or suppressible cytochrome P450 - by screening for drugs which reduce the catabolism of retinoic acid, useful in cancer chemotherapy and the treatment of acne and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protease binding site; protease; protease indicator; fluorescent signal; detection; protease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is a degenerate peptide from which the PCR primer used in the amplification process is derived. The PCR involves the inducible cytochrome P450 gene which produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. A form of cytochrome P450 is P450RAI which specifically metabolises a derivative of retinoic acid (RA). It is highly induced by RA in cell lines and tissues. This allows for the development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA
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                                                                                                                                               Degenerate peptide; PCR; amplification; cytochrome P450 gene; oxidative metabolism; P450RAI; retinoic acid; RA; promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide containing a protease binding site.
                                                                                                       Cytochrome P450 degenerate primer 2.
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96US-00724466.
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                                                            (first entry)
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Best Local Similarity
Matches 2; Conserv
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                                                            07-JUL-1998
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                                                                                                                                                                                                                Synthetic.
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                    AAW37726;
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98WO-US006690. 97US-0043047P

03-APR-1998; 04-APR-1997;

JS5714342-A

Synthetic

RESULT 10

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03-FEB-1998

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WO9844945-A1

15-OCT-1998.

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AAW87481 to AAW87486 represent human immunodeficiency virus-1 (HIV-1) sequences in Mo/LAI cells that were used for comparing the mutant amino cid sequences of the defective HIV provirus in L-2 cells. AAV1858 to AAV1853 represent the portions of pol protease (prot.), vpr. env (gpl20 and gp41), and nef gene regions that were mutated as compared to wild-type HIV-1 in LAI or Mo/LAI cells. The invention relates to mutated DNA, proteins or fragments of defective HIV-1 provirus in L-2 cell line. The mutations result in non-infectious HIV-1 particles. Inactive, protease-corping appropriate in HIV-1 particles. Inactive, protease-corping appropriate in HIV-1 sero-negative or -positive subjects, specifically those with HIV-1 sero-negative or -positive subjects, specifically those with HIV-1 infection, both for prevention and treatment. Fragments of nef gene and fragments encoding specific mutant of met gene and fragments encoding specific mutant corresponding mutant proteins are detected in immunoassays using corresponding mutant proteins are detected in immunoassays using corresponding attached to a radioisotope, chemotherapeutic agent or toxin, can be used to reduce the severity of HIV infections. (Updated on 17-OCT-can be used to reduce the severity of HIV infections. (Updated on 17-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus-1; HIV-1; protease; provirus; L-2 cell;
mutation; Nef protein; immunogen; apoptosis; treatment; hybridisation;
cell lysis; chemotherapeutic; toxin; HIV infection.
                                                                                                                                       New nucleic acid encoding mutant or truncated forms of human immune deficiency virus proteins - used to generate non-infectious particles useful as therapeutic or prophylactic immunogens, also for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 10; DB 2; Length 4; 100.0%; Pred. No. 2e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV-1 mutant env gp120 amino acid fragment in L-2 cell.
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                                                                                                                                                                                                                      Example 1; Fig 1; 66pp; English.
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               (IMMU-) IMMUNE RESPONSE CORP.
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Matches 2; Conservative
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                                                                                        WPI; 1998-568304/48.
                                                                                                            N-PSDB; AAV71866.
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Misc-difference
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11-FEB-1999
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AAW87477
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the defective human immunodeficiency virus-1 (HIV-1) provirus in L-2 cells. They represent the portions of pol protease (prot.), vpr. env cells. They represent the portions of pol protease (prot.), vpr. env cells. They represent the portions of pol protease (prot.), vpr. env (gp120 and gp41), and enf gene regions that were mutated as compared to wild-type HIV-1 in LAI or MO/LAI cells. The invention relates to mutated to mutations result in non-infectious HIV-1 particles containing at least one of Nef truncated protein fragments are used as immunogens, particularly for truncated protein fragments are used as immunogens, particularly for reducing or preventing apoptoas in HIV-1 sero-negative or -positive conjugation or preventing apoptoas in HIV-1 infection, both for prevention and treatment. Fragments of nef gene and fragments encoding specific and treatment. Fragments of nef gene and fragments encoding specific mutant Nef proteins are also useful in hybridisation tests for diagnostic corresponding mutant protein are detected in immunoassays using antibodies. The protease-deficient HIV-1 particles and antibodies, contionally attached to a radioisotope, chemotherapeutic agent or toxin, coptionally attached the severity of HIV infections. (Updated on 17-OCT-
2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-P; presentilin I; presentilin II; cellular tumour antigen; glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-I; bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A.
                                                                                                                                                                                        New nucleic acid encoding mutant or truncated forms of human immune deficiency virus proteins - used to generate non-infectious particles useful as therapeutic or prophylactic immunogens, also for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                            Sequences AAW87475 to AAW87463 represent mutant amino acid sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human semaphorin III mutant protein fragment 16.
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                                                                                                                                                                                                                                                                                       Example 1; Fig 1; 66pp; English
97US-0043047P
                                         (IMMU-) IMMUNE RESPONSE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUL-1999 (first entry)
                                                                                                                                   WPI; 1998-568304/48.
                                                                                                                                                          N-PSDB; AAV71860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4 AA;
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04-APR-1997;
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15-OCT-1998,

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The present sequence represents an immunisation motif normally excluded, but which may be used with advantage for tolerisation by itself or in conjunction with other epitope sequences from the present invention. The present invention describes a polypeptide comprising a human myelin basic protein (hMBP) fragment including P89-101 of hMBP, excluding native hMBP. The term P89-101 is not defined but may be intended to mean amino acids 89-101 of hMBP. The polypeptide can be used for tolerising a mammalian host immune system comprising and T cells to an immunogen of interest, wherein said immunogen is restricted by a transplantation antigen of said host. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-
                                                                                                                                                                                             Polypeptide comprising human myelin basic protein fragment - useful as immuno modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalian Ii key peptide; mammalian invariant chain protein; allergy;
immune response; MHC class II; antigenic; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 10; DB 2; Length 4; 100.0%; Pred. No. 2e+06; .ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE101 analogue effector compound SEQ ID NO:26.
                                                                  (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                    Disclosure; Page 8; 8pp; English
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87US-00086694
                       88EP-00307608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Conservative
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                                                                                                            Steinman L, Zamvil S;
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                                                                                                                                                        WPI; 1998-034664/04
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Best Local Similarity
Matches 2; Conserv
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUN-1997;
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  17-AUG-1987;
                       17-AUG-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW47950;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related disease, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, and high selerosis, alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated protein 2 (MAP2), neurofilament-M, neurofilament-F, presentiin I, presentiin II, glial fibrillary acidic protein (GRAP), the cellular tumour antigen ps; Hecell leukemia/lymphoma 2 (bcl-2) prote-oncogene, semaphorin III, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A
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                                                                                                                                                                                                                                                                                                         Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type RNA.
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                                                                                                                                                                                                    Burbach JPH;
                                                                                                            (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
(UYRO-) UNIV ROTTERDAM ERASMUS.
(UYUT-) RIJKSUNIV UTRECHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunisation motif associated with PLP 7.
                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 16; 258pp; English.
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                                                                                                                                                                                                    Van Leeuwen FW, Grosveld FG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97EP-00106788.
                         98WO-IB000705
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                                                                                                                                                                                                                                             WPI; 1998-609901/51.
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Best Local Similarity
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                         02-APR-1998;
                                                                     10-APR-1997;
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08-JUL-1998
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modulation of immune response, e.g. for treating malignant, allergic autoimmune disease or allograft rejection.
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Example 1; Page 27; 149pp; English.

The present sequence represents an AE101 analogue effector compound used in the present invention. The present invention describes a mammalian invariant chain protein (Ii) key peptide of sequence LRMKLPKPEKVSKMR and modifications with the exclusion of peptide YRMKLPKPPKPSKNR. WHC class II molecules are synthesised in the endoplasmic reticulum with their antigenic peptide sites blocked by the invariant chain protein (Ii). The products and method can be used for the modulation of an immune response for therepoutic or diagnostic purposes. The enhancement of immunity can be used in the treatment of e.g. mailgnant or allergic disease. The immunosuppression can be used for the treatment of autoimmune disease, e.g. rheumatoid arthritis, multiple sclerosis, diabetes mellitus, lupus erythematosus, and psoriasis or allograft rejection 

Sequence 4 AA;

.; 0 0; Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels

1 RM 2 | | 2 RM 3

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Search completed: February 28, 2006, 08:45:08 Job time : 2.68505 secs

75, Appl 77, Appl 78, Appl 173, App 46, Appl 13, Appl 4, Appli 90, Appli

Sequence

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OM protein

Run on:

Sequence:

Title: Perfect

Searched:

Database

Result

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GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
ITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 10; DB 1; Length 3; 100.0%; Pred. No. 4.6e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATR:
APPLICATION NUMBER: US/08/968,676
US-08-350-260A-413

US-08-818-253-58

US-09-020-880-75

US-09-020-880-77

US-09-020-880-77

US-09-120-880-77

US-09-131-96A-13

US-09-191-96A-9

US-09-101-649-13

US-08-930-921-4

US-08-818-111-91

US-08-818-111-91

US-08-818-111-91

US-09-101-544-75

US-09-101-544-77

US-09-101-544-77

US-09-101-544-77

US-09-101-544-77

US-09-101-544-77
                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C. STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/08968676 Patent No. 5919639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
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TOPOLOGY: linear
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                                                                                                                  (without alignments)
960.804 Million cell updates/sec
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                                                                                                   February 28, 2006, 08:53:26; Search time 0.172097 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                 GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                        572060
                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgm2_6/prodata/1/iaa/5_COMB.pep:*
/cgm2_6/prodata/1/iaa/6_COMB.pep:*
/cgm2_6/prodata/1/iaa/FCOMB.pep:*
/cgm2_6/prodata/1/iaa/PCTUS_COMB.pep:*
/cgm2_6/prodata/1/iaa/RE_COMB.pep:*
/cgm2_6/prodata/1/iaa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-101-649-12
US-09-055-075C-16
US-09-055-075C-18
US-09-396-813-3
US-09-919-124-18
US-09-919-124-18
US-09-6256-237-23
US-09-256-237-23
US-09-763-293A-30
US-09-763-293A-31
US-09-763-293A-31
US-09-763-293A-31
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S-09-191-906A-2
S-09-101-649-12
S-09-055-075C-16
S-09-356-813-3
S-09-919-124-16
                                                                                                                                                                                                                                                                                    Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-08-968-676-25
                                                                                                                                                      US-10-717-665A-44_COPY_448_449
                                                                                                                                                                                                                                                           572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                        Issued Patents AA:
                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                            Copyright
                                                                                                                                                                                      1 RM 2
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Match
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1000.0
1000.0
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                                                                                                                                                                            score:
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Gaps

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MOLECULE TYPE: peptide
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US-08-331-383-4
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                                               US-09-261-894A-27
Sequence 27, Application US/09261894A
Sequence 27, Application US/09261894A
Sequence 27, Application US/09261894A
Sextent No. 6835382
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT E.
APPLICANT: ADAMS, SHARLENE
APPLICANT: ADAMS, SHARLENE
CURRENT: XU, MINCHEN
FILLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION
CURRENT APPLICATION UMBER: US/09/261,894A
CURRENT FILLNG DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 27
LENGTH: 3
LENGTH: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Komoriya, Akira
APPLICANT: Romoriya, Akira
APPLICANT: Romoriya, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of
TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
COTER INFORMATION: Description of Artificial Sequence: Synthetic;
COTER INFORMATION: peptide
CS-09-261-894A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,383
FILING DATE: 28-OCT-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 10; DB 2; I
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 2; Conservative 0; Mismatches 0;
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NAME: Dow, Karen B.
REGIESTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 16865
RELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPAK: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08331383
Patent No. 5605809
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UN
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Sequence 4, Application US/08549008

Patent No. 5714342
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fackard, Beverly S.
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of
TITLE OF INVENTION: Compositions for the Detection of
TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE California
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Ouery Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC Compatible
COMPUTER: IMP PC Compatible
COMPUTER: IMP PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,008
FILING DATE: 27-0CT-1995
CLASSIFICATION NUMBER: US 08/331,383
FILING DATE: 28-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber: Blen Lauver
REGISTRATION NUMBER: 32,762
REPRENCE/DOCKET NUMBER: 32,762
REPRENCE/DOCKET NUMBER: 32,762
REPRENCE/DOCKET NUMBER: 32,762
REPRENCE/DOCKET NUMBER: 35,762
RELEPHONE: (415) 576-0300
TELLEPHONE: (415) 576-0300
TELLEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5

20.08-968-676-26

; Sequence 26, Application US/08968676

; Patent No. 5919639

; GENERAL INFORNATION:

; APPLICANT: Humphreys, Robert E

, non:ICANT: Adams, Sharlene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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APPLICANT: Nachman, Ronald J
APPLICANT: Nachman, Ronald J
APPLICANT: Garside, Christopher S
APPLICANT: Tobe, Stephen S
TITLE OF INVENTION: Mimetic Insect Allatostatin Analogs for Insect Control
FILE REFERENCE: P.C. 0047.99-Ronald J. Nachman et al.
CURRENT APPLICATION NUMBER: US/09/191,906A
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
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Andersen, Thomas T.
Bizios, Rena
TITLE OF INVENTION: Peptides for
Altering Osteoblast Adhesion
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENČE ADDRESS:
ADDRESSEE: Heslin & Rothenberg, P.C.
STREET: 5 Columbia Circle
CITY: Albany
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
    DE 197 01 141.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09191906A Patent No. 6207643 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09101649
Patent No. 6262017
GENERAL INFORMATION:
                                                                                 31,298
                                                                                                  REFERENCE/DOCKET NUMBER: 0:
TELECOMMUNICATION INFORMATION
TELEPHONE: (202)672-5300
TELEFRAX: (202)672-5399
                         FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G:
REGISTRATION NUMBER: 31,29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Diploptera punctata
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Conservative
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Best Local Similarity 100.
Matches 2; Conservative
                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                             LENGTH: 4 amino acids
      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS:
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Best Local Similarity
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US-09-191-906A-2
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                                                                                                                                                                   TELEFAX:
TELEX: 9
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APPLICANT: Mueller, Rolf
APPLICANT: Mueller, Rolf
APPLICANT: Mueller, Rolf
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR EXPRESSING
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
COUNTRY: USA
ZIP: 2007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATENIT Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0,
TOTRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,308
FT.ING DATE: 16-JAN-1998
                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.6e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/09008308
Patent No. 6080575
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
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TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RM 3
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                                                                                                                                                               COUNTRY:
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Gaps

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Gaps

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Sequence 15. Application US/09919124

Facent No. 6557296

GENERAL INFORMATION:

APPLICANT: Lufting, Ronald B.

TITLE OF INVENTION: No. 6557296-Infectious, Protease Defective HIV Particles and
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Therefor
FILE REFERENCE: PIM 4867

CURRENT APPLICATION NUMBER: US/09/919,124

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/043,047
                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Luftig, Ronald B.
TITLE OF INVENTION: No. 6328976-Infectious, Protease Defective HIV Particles and
TITLE OF INVENTION:
Nucleic Acid Molecules Encoding Therefor
TITLE OF INVENTION:
NUMBER: 1938-04-03
CURRENT PILING DATE: 1938-04-04
NUMBER: 60/043,047
PRIOR APPLICATION NUMBER: 60/043,047
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Modified mouse; OTHER INFORMATION: Ii key peptide US-09-396-813-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09396813
; Sequence 3, Application US/09396813
; Patent No. 6432409
; GENERAL INFORMATION:
    APPLICANT: Humphreys, Robert E.
    APPLICANT: Adams, Sharlene
; APPLICANT: Xu, Minchen
; TITLE OF INVENTION: HYBRID PEPTIDES MODULATE THE IMMUNE RESPONSE
; FILE REPERENCE: REHAZOO7
; CURRENT APPLICATION NUMBER: US/09/396,813
; CURRENT FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4
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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ; ORGANISM: Human immunodeficiency virus type 1 US-09-055-075C-18
US-09-055-075C-18; Sequence 18, Application US/09055075C; Patent No. 6328976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
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US-09-919-124-16
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US-09-055-075C-16

Sequence 16, Application US/09055075C

Patent No. 6328976

APPLICANT: Luftig, Ronald B.

TITLE OF INVENTION: Nucleic Acid Molecules Encoding Therefor

TITLE OF INVENTION: Nucleic Acid Molecules Encoding Therefor

TITLE OF INVENTION: Nucleic Acid Molecules Encoding Therefor

TITLE OF INVENTION: Nucleic Acid Molecules Encoding Therefor

CURRENT APPLICATION NUMBER: US/09/055,075C

CURRENT FILING DATE: 1998-04-03

PRIOR FILING DATE: 1997-04-04

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16
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                                                                                                          CURELING DATE: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: DTK Grafika 486
COMPUTER: DTK Grafika 486
COMPUTER: MAS-DOS 5.0
SOFTWARE: WAS-DOS 5.0
SOFTWARE: WAS-DOS 5.0
SOFTWARE: WAS-DOS 5.0
SOFTWARE: WAS-DOS 5.0
FILING DATE: 14-JU1-1998
PRIOR APPLICATION NUMBER: 60/010,026
FILING DATE: 16-JAN-1996
APPLICATION NUMBER: 60/029,189
FILING DATE: 31-OCT-1996
ATTORNEY AGENT INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hansen, Philip E.
REGISTRATION NUMBER: 32700
REGISTRATION NUMBER: 0094.026BWO
RELECOMMUNICATION INFORMATION:
TELEPHONE: (518) 452-5600
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: yes
SEQUENCE DESCRIPTION: SEQ ID NO: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                     ZIP: 12203
COMPUTER READABLE FORM:
                  STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RM 3
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Gaps

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RESULT 10

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Sequence 23, Application US/09256237
Patent No. 6670147
GENERAL INFORMATION:
APPLICANT: Heidtmann, Hans H.
Mueller, Rolf
Sedlacek, Hans-Harald
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR EXPRESSING
ACTIVE SUBSTANTES WHICH CAN BE ACTIVATED BY PROTEASES, AND
PREPARATION AND USE
                          Gaps
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                        Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  Pred. No. 4.6e+05; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 10; DB 2; ilarity 100.0%; Pred. No. 4.6e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 026083/0189
TELECOMMUICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/008,308
FILING DATE: 16-JAN-1998
APPLICATION NUMBER: DE 197 01 141.1
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/256,237
FILING DATE: 24-Feb-1999
CLASSIFICATION: <UNKNOWD>
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FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
100.08;
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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                        2; Conservative
  Best Local Similarity
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US-09-256-237-23
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Luftig, Ronald B.
TITLE OF INVENTION: No. 6557296-Infectious, Protease Defective HIV Particles and
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Therefor
FILE REFERENCE: P-IM 4867
CURRENT APPLICATION NUMBER: US/09/919,124
CURRENT FILING DATE: 1001-07-30
PRIOR PLILING DATE: 1997-04-04
PRIOR FILING DATE: 1997-04-04
PRIOR PLILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
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Patent No. 6664371
GENERAL INFORMATION:
APPLICANT: Nachman, Ronald J
APPLICANT: Garside, Christopher S
APPLICANT: Tobe, Stephen S
TITLE OF INVENTION: Mimetic Insect Allatostatin Analogs for Insect Control
FILE REFERENCE: P.C. 0047.99-Ronald J. Nachman et al.
CURRENT APPLICATION NUMBER: US/09/680,201
CURRENT FILING DATE: 2001-01-19
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100.0%; Pred. No. 4.6e+05;
tive 0; Mismatches 0;
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                                                                                                                               ; LENGTH: 4
; TYPE: RRT
; OGGANISM: Human immunodeficiency virus type 1
US-09-919-124-16
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US-09-919-124-18
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                        09/055,075
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Patent No. 6557296
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SOFTWARE: Patentin Ver. 2.1
FINAME:
PRIOR FILING DATE: 1997-04-04
PRIOR APPLICATION NUMBER: US 09,
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 16
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Best Local Similarity 100.0
Matches 2; Conservative
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Best Local Similarity 100.0
Matches 2; Conservative
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Length 4:

DB 2;

100.0%; Score 10;

Query Match

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46, Appl
67, Appl
73, Appl
79, Appl
85, Appl
127, App
139, App
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Publication No. US20030207324A1
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Sharlene
APPLICANT: Adams, ImmunoTHERAPY BY MODULATION OF ANTIGEN
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSES:
CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 10; DB 3; Length 3; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/261,894
FILING DATE: March 3, 1999
CLASSIFICATION:
US-09-192-854-77
US-09-192-864-108
US-09-751-1008-46
US-09-968-561A-73
US-09-968-561A-73
US-09-968-561A-191
US-09-968-561A-191
US-09-968-561A-137
US-09-968-561A-137
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US-09-968-561A-187
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US-09-968-561A-217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REPERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Conservative
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Matches 2; Conserv
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31, Appl
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1433.071 Million cell updates/sec
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                                                                                                                                        February 28, 2006, 08:54:36; Search time 0.583124 Seconds
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Sequence 48, Al
Sequence 3, Al
Sequence 8, Al
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Sequence 18,
Sequence 10,
Sequence 48,
Sequence 3, A
Sequence 86,
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-022-717-48
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US-10-163-198-86
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Perfect score:
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
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      100.0%; Score 10; DB 3; Length 4; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
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US-09-984-91-10
Sequence 10, Application US/09988491
Sequence 10, Application US/09988491
Publication No. US20030166529A1
GENERAL INPORMATION:
APPLICANT: Mileusnic, Radmilla
APPLICANT: Mileusnic, Radmilla
APPLICANT: Rose, Stephen Peter Russell
TITLE OF INVENTION: Polypeptides and their Uses
TITLE OF INVENTION NUMBER: US/09/998,491
CURRENT FILING DATE: 2001-11-30
PRIOR PILING DATE: 2001-11-30
PRIOR PLILNG DATE: 2001-04-18
PRIOR PLILNG DATE: 2001-04-18
PRIOR PLILNG DATE: 2001-04-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
TENNOW.
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100.0%; Pred. No. 1.7e+06;
tive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Lag 2; Conservative
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Matches 2; Conserv
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US-09-919-124-16

Sequence 16, Application US/09919124

Patent No. US20020061313A1

GENERAL INFORMATION:

APPLICANT: Luffig, Ronald B.

TITLE OF INVENTION: No. US20020061313A1-Infectious, Protease Defective HIV Particles

TITLE OF INVENTION: Nucleic Acid Molecules Encoding Therefor

FILE REPERENCE: P-14 4867

CURRENT APPLICATION NUMBER: US/09/919,124

CURRENT FILING DATE: 2001-07-30

PRIOR FILING DATE: 1997-04-04

PRIOR FILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 4
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                                                                                Sequence 31, Application US/0848409
Publication No. US20020076412A1
GENERAL INFORMATION:
APPLICANT: Steinman, Lawrence
APPLICANT: Zamvil, Scott
TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4;
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COUNTRY: USA 22

ZIP: 98104-7092

COMPUTER READABLE FORM: MEDIUM TYPE: FALOPY disk COMPUTER: IBM PC COMPATION: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATE: 07-JUN-1995

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY AGENT INFORMATION: NAME: Maki, David J. REFERENCE/DOCKET NUMBER: 690068.409C1

TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION FOR SEQ ID NO: 31: SEQUENCE CHARACTER STREET CS: 12060 682-6031

INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTER STREET CS: 12060 682-6031

INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTER STREET CS: 12060 882-6031
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100.0%; Score 10; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4 amino acids
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Gaps

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Sequence 86, Application US/10163198

Sequence 86, Application WJ/10163198

Publication No. US20030126645A1

GENERAL INFORMATION:

APPLICANT: Rebecca E. Cahon;

APPLICANT: Elmer P. Heppard

APPLICANT: Hajime Sakai

TITLE OF INVENTION: Alteration Of Embryo/Endosperm Size During Seed Development;

FILE REFERENCE: BB1487 US NA

CURRENT APPLICATION NUMBER: 60/295,921

FRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

SOFTWARE: Microsoft Office 97

SEQ ID NO 86

LENGTH: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Humphreys, Robert E.
APPLICANT: Adams, Sharlene
APPLICANT: Adams, Sharlene
APPLICANT: Adams, Sharlene
APPLICANT: AN MIAZHEN
TITLE OF INVENTION: HYBRID PEPTIDES MODULATE THE IMMUNE RESPONSE
FILE REFERENCE: REH2007
CURRENT EPLING DATE: 202-07-17
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 3
LENGTH: 4
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                                                                                                            CTHER INFORMATION: LRMS Insert US-10-032-717-48
                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100...
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SEQ ID NO 48
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APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
FRIOR APPLICATION NUMBER: 60/242,838
FRIOR APPLICATION UNMBER: 60/242,838
FRIOR APPLICATION UNMBER: 60/242,838
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                 APPLICANT: Humphreys, Robert B
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
WUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/261,894
FILING DATE: March 3, 1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..7e+06;
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                                                                                                                                                                                                                                                                                             ADDRESSEE: Kevin M. Farrell, P.C. STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
                                                                               Sequence 26, Application US/09261894
Publication No. US20030207324A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 48, Application US/10032717
Publication No. US20020151709A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35.505
REFRENCE/DOCKET NUMBER: REH-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0528
INFORMATION POR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Peng
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -10-032-717-48
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US-10-245-871-8
US-10-245-871-8
US-10-245-871
Sequence 8, Application US/10245871
Publication No. US20030235594A1
Publication No. US20030235594A1
Publication No. US20030235594A1
Publication No. US20030235594A1
APPLICANT: HUMPHERS ROBERT
APPLICANT: XU, MINZHEN
PAPLICANT: XU, MINZHEN
PILE REFERENCE: REH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2003-01-09
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LEASTH: 4
LEASTH: 4
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APPLICANT: HUMPHREYS:

APPLICANT: HUMPHREYS:

APPLICANT: HUMPHRENS:

TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES:

TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES:

TILE REFERENCE: REH-2013

CURRENT APPLICATION NUMBER: US/10/245,871

PRIOR FILING DATE: 2002-07-17

PRIOR FILING DATE: 2002-07-17

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 905

SOFTWARE: PATCHLIN VET: 2.1

SOFTWARE: PATCHLIN VET: 2.1
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                               Sequence 3, Application US/10245871; Publication No. US20030235594A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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APPLICANT: NIGHOUSE D. DOON
APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Iyun E. Stranger Bencoding No. US2003017528A1el Proteins With
TITLE OF INVENTION: Peeticidal Activity Against Coleopterans
TITLE OF INVENTION: Peeticidal Activity Against Coleopterans
TITLE OF INVENTION NUMBER: US/10/414,637
CURRENT FILING DATE: 2003-04-16
PRIOR FILING DATE: 2001-10-23
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
SOFTWARE: PEECE OF SEQ ID NOS: 48
SOFTWARE: PEECE OF SEQ ID NOS: 48
SOFTWARE: PEECE OF SEQ ID NOS: 48
SOFTWARE: PEECE OF WINDOWS VERSION 4.0
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Sequence 2, Application US/10385317
Sequence 2, Application No. US20030161857A1
GENERAL INFORMATION: Ronald 3
APPLICANT: Nochman, Ronald 4
APPLICANT: Tobe, Stephen S
APPLICANT: Tobe, Stephen S
TITLE OF INVENTION: Mimetic Insect Allatostatin Analogs for Insect Control FILE REFERENCE: P.C. 0047.99-Ronald J. Nachman et al.
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.70+06;
Matches 2; Conservative 0; Mismatches 0; Indels
                                       Length 4;
                                                                                   0; Indels
                                         100.0%; Score 10; DB 4; L
100.0%; Pred. No. 1.7e+06;
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Sequence 48, Application US/10414637
Publication No. US20030177528A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Wicholas B. Duck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: LRMS INSERT US-10-414-637-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT (CRANISM: Diploptera punctata US-10-385-317-2
                                                Query Match
Best Local Similarity 100.
Matches 2; Conservative
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US-10-659-509-2

US-10-659-509-2

§ Sequence 2, Application US/10659509

§ Publication No. US20040039159A1

§ GENERAL INFORMATION:

§ APPLICANT: Nachman, Ronald J

§ APPLICANT: Tobe, Stephen S

§ TITLE OF INVENTION: Mimetic Insect Allatostatin Analogs for Insect Control

§ TITLE OF INVENTION: Wimber: US/10/659,509

© CURRENT APPLICATION NUMBER: US/10/659,509

© CURRENT FILING DATE: 2003-09-10

§ NUMBER OF SEQ ID NOS: 14

§ SEQ ID NO 2

LENGTH: 4
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RESULT 14
US-10-45-91-801

Sequence 801, Application US/10245871

Sequence 801, Application US/10245871

Publication No. US20332594A1

GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT

APPLICANT: KU, MINZHEN

TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

FILE REPERENCE: REH-2013

CURRENT APPLICATION NUMBER: US/10/245,871

CURRENT FILING DATE: 2003-01-09

PRIOR FILING DATE: 2002-07-17

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 905

SOFTWARE: Patentin Ver. 2.1

LENGTH: 4
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CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Ii-key/Ebola virus VP24 MHC Class II epitope
OTHER INFORMATION: hybrid peptide
FEATURE:
OTHER INFORMATION: C-term amidated
US-10-245-871-801
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; ORGANISM: Diploptera punctata
US-10-659-509-2
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Search completed: February 28, 2006, 09:02:03 Job time : 1.58312 secs

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Sequence 801, App
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Sequence 9, Appli
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Sequence 8, Appli
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556.876 Million cell updates/sec
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                                                                                                                       February 28, 2006, 08:56:26; Search time 0.053467 Seconds
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2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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10	100.0	7	US-11-244-209-20	Sequence		_
10	100.0	7	US-11-247-423-459	Sequence	459, App	Ω
10	100.0	8	US-10-980-346B-43	Sequence	43, App	_
10	100.0	60	US-11-045-024-1087	Sequence	1087, A	Q,
10	100.0	80	US-11-045-024-1088	Sequence	1088, A	Ω.
10	100.0	80	US-11-045-024-1089	Sequence	1089, A	Ω
10	100.0	00	US-11-045-024-1090	Sequence	1090, A	Q,
10	100.0	80	US-11-045-024-1091	Sequence	1091, A	Ω
10	100.0	60	US-11-045-024-1679	Sequence	1679, A	Q.
10	100.0	80	US-11-045-024-2508	Sequence	2508, Ap	Ω.
10	100.0	60	US-11-045-024-2509	Sequence	2509, A	Δ.
10	100.0	60	US-11-045-024-2510	Sequence		α
10	100.0	60	US-11-045-024-3503	Sequence	_	α
10	100.0	σο	US-11-045-024-3504	Sequence	3504, A	Ω
10	100.0	60	US-11-045-024-3505	Sequence	3505, A	Ω
10	100.0	60	US-11-045-024-3506	Sequence	3506, Ap	Д
10	100.0	80	US-11-045-024-4032	Sequence	4032, A	Q,
10	100.0	α	US-11-045-024-4033	Sequence	4033, A	Д
10	100.0	00	US-11-045-024-4034	Sequence	4034, A	Ω
10	100.0	60	US-11-045-024-4369	Sequence	4369, A	Д

## ALIGNMENTS

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APPLICANT: POON, LIT MAN
APPLICANT: GUAN, XI
APPLICANT: GUAN, XI
APPLICANT: GUAN, XI
APPLICANT: GUAN, XI
APPLICANT: GUAN, XI
APPLICANT: NICHOLLS, JOHN M.
APPLICANT: LEUNG, FREDERICK C.
TITLE OF INVENTION: THEREOF
FILE REFERENCE: V0690.0031
CURRENT FILING DATE: 2004-07-21
NUMBER OF SEQ ID NOS: 2918
SOFTWARE: Patentin version 3.2
SEQ ID NO 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/11033039
Publication No. US20060002947A1
GENERAL INPORMATION:
APPLICANT: HUMPHREVS, ROBERT
APPLICANT: KU, MINZHEN
TITLE REFERENCE: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017USO USD5-01-11
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT PILING DATE: 2005-01-11
PRIOR FILING DATE: 2002-09-17
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR APPLICATION NUMBER: 10/197,000
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            Sequence 1660, Application US/10895064 Publication No. US20060018923A1 GENERAL INFORMATION:
                                                                                     APPLICANT: PEIRIS, JOSEPH S.M.
APPLICANT: YUBN, KWOK YUNG
APPLICANT: POON, LIT MAN
APPLICANT: GUAN, YI
APPLICANT: CHAN, KWOK HUNG
APPLICANT: NICHOLLS, JOHN M.
APPLICANT: LEUNG, FREDERICK C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Corononavirus-HKU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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JS-10-895-064-1660
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US-11-033-039-3
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1 RM 2
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US-10-895-064-2685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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APPLICANT: HUMPHERS, ROBERT
APPLICANT: HUMPHERS, RIL-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
TITLE OF INVENTION: L1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-20170801
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR FILING DATE: 2002-09-17
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                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Modified ; OTHER INFORMATION: mammalian li-key peptide US-11-033-039-3
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                                                                                                                                                                                                                                                                                                                               100.0%; Score 10; DB 7; Length 4; 100.0%; Pred. No. 8.2e+04;
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100.0%; Pred. No. 8.2e+04;
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PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: Patentin version 3.3
SEQ ID NO 3
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 2; Conservative
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Best Local Similarity 100.
Matches 2; Conservative
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APPLICANT: PERRIS, JOSEPH S.M.
APPLICANT: PUEN, KWOK YUNG
APPLICANT: YUEN, KWOK YUNG
APPLICANT: GUAN, YI
APPLICANT: CHAN, KWOK HUNG
APPLICANT: LEUNG, FREDERICK C.
APPLICANT: LEUNG, FREDERICK C.
TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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| Sequence 1660, Application US/11129741
| Publication No. US20060034853A1
| GENERAL INPORMATION:
| APPLICANT: VUEN, KWOK YUNG
| APPLICANT: LAD, KAR PUI SUSANNA
| APPLICANT: CHAN, KAR PUI SUSANNA
| APPLICANT: CHAN, KAR PUI SUSANNA
| APPLICANT: CHAN, KAR PUI SUSEHH S.M.
| APPLICANT: PETRIS, JOSEPH S.M.
| APPLICANT: PETRIS, JOSEPH S.M.
| APPLICANT: PETRIS, USEPH S.M.
| APPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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COTHER INFORMATION: Description of Artificial Sequence: Synthetic
FOTHER INFORMATION: hybrid peptide
1.013-039-801
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Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indel
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; sequence 2685, Application US/10895064; Publication No. US20060018923A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Corononavirus-HKU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
....hes 2; Conservative
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Gaps

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APPLICANT: Wang, Xiaoju
TITLE OF INVENTION: Phage Microarray Profiling of the Humoral Response to Disease
FILE REFERENCE: UM-09899
CURRENT APPLICATION NUMBER: US/11/145,861
CURRENT FILING DATE: 2005-06-06
NUMBER OF SEQ ID NOS: 464
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/11033039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHRENS, ROBERT
APPLICANT: HUMPHRENS', ROBERT
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REPERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT PILING DATE: 2005-01-11
PRIOR FILING DATE: 2002-09-17
PRIOR FILING DATE: 2002-09-17
PRIOR FILING DATE: 2002-09-17
PRIOR FILING DATE: 2002-09-14
PRIOR FILING DATE: 1999-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Modified OTHER INFORMATION: mammalian li-key peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 10; DB 7; Length 5; 100.0%; Pred. No. 8.2e+04; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                          100.0%; Score 10; DB 7; I
100.0%; Pred. No. 8.2e+04;
iive 0; Mismatches 0;
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
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Publication No. US20060014138A1
GENERAL INFORMATION:
APPLICANT: Chinnaiyan, Arul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 1452
SOFTWARE: Patentin version 3.3
SEQ ID NO 9
LENGTH: S
                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                    ; OTHER INFORMATION: Synthetic US-11-191-574-9
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Best Local Similarity 100.
Matches 2; Conservative
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Matches 2; Conservative
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LOCATION: (5)..(5)
OTHER INFORMATION: Ava
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                                                                         LENGTH:
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
TITLE OF INVENTION: ADVOINGNER: 20/10/20,186
CURRENT APPLICATION NUMBER: US/11/062,186
CURRENT PLING DATE: 2005-02-18
PRIOR PILING DATE: 2004-02-18
PRIOR PILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 20
TENGTH: 6
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APPLICANT: Bgel-Mitani, Michi
APPLICANT: Bgel-Mitani, Michi
APPLICANT: Balschmidt, Per
APPLICANT: Balschmidt, Per
APPLICANT: Diers, Ivan
APPLICANT: Diers, Ivan
APPLICANT: Diers, Ivan
APPLICANT: Diers, Ivan
APPLICANT: Diers, Ivan
APPLICANT: Diers, Ivan
APPLICANT: Diers, Ivan
APPLICANT: Diers, Ivan
CURRENT APPLICATION NUMBER: US/11/191,574
CURRENT APPLICATION NUMBER: US/10/205,270
PRIOR APPLICATION NUMBER: PA 2001 01140
PRIOR APPLICATION NUMBER: PA 2001 01140
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-34
PRIOR FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                             Length 5;
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                                          CURRENT APPLICATION NUMBER: US/10/895,064
CURRENT FILING DATE: 2004-07-21
NUMBER OF SEQ ID NOS: 2918
SOFTWARE: Patentin version 3.2
SEQ ID NO 2685
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/11062186
Publication No. US20050272097A1
GENERAL INFORMATION:
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Publication No. US20050272125A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                          TYPE: PRT; ORGANISM: Corononavirus-HKU1
US-10-895-064-2685
  TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 2; Conservative
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Matches 2; Conservative
                         FILE REFERENCE: V0690.0031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-11-062-186-20
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PRIOR APPLICATION NUMBER: 60/393,211
PRIOR APPLICATION NUMBER: 60/393,211
PRIOR FILING DATE: 2002-07-01
PRIOR FILING DATE: 2002-07-01
PRIOR FILING DATE: 2002-07-01
PRIOR PLICATION NUMBER: 60/393,233
PRIOR PLICATION NUMBER: 60/393,235
PRIOR PLILING DATE: 2002-07-01
PRIOR PLILING DATE: 2002-07-01
PRIOR PLILING DATE: 2002-07-01
PRIOR PLILING DATE: 2002-07-01
PRIOR PLILING DATE: 2002-07-01
PRIOR PLILING DATE: 2002-12-04
PRIOR PLING DATE: 2002-12-04
PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/430,948
PRIOR PLING DATE: 2002-12-04
PRIOR PLING DATE: 2002-12-04
PRIOR PLING DATE: 2002-12-04
PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/430,948
PRIOR PRIOR SEQ ID NOS: 614
SOFTWARE: PARCHIN VERSION 3.2
SOFTWARE: PARCHIN VERSION 3.2
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Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels
FILING DATE: 2002-07-01
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-11-249-847-51
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Sequence 51, Application US/11249847

Sequence 51, Application US/11249847

Publication No. US20060035270A1

GENERAL INFORMATION:

APPLICANT: Chan, John W.

APPLICANT: Chan, John W.

APPLICANT: Chan, John W.

APPLICANT: Chan, John W.

APPLICANT: Chan, John W.

APPLICANT: Chan, John W.

APPLICANT: Chan, John W.

APPLICANT: Chan, John W.

APPLICANT: Chan, John W.

APPLICANT: Chan, John W.

TITLE OF INVENTION: PROTEIN ANALYSIS

FILE REFERENCE: ETH-P05-001

CURRENT APPLICATION NUMBER: US/11/249,847

CURRENT FILING DATE: 2005-10-12

PRIOR APPLICATION NUMBER: 60/379,626

PRIOR APPLICATION NUMBER: 60/379,626

PRIOR APPLICATION NUMBER: 60/379,137

PRIOR APPLICATION NUMBER: 60/393,137

PRIOR APPLICATION NUMBER: 60/393,137

PRIOR APPLICATION NUMBER: 60/393,197
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Sequence 2685, Application US/11129741

Sequence 1080060034853A1

GENERAL INFORMATION:

APPLICANT: WOO, CHIU YAT PATRICK

APPLICANT: LAU, KAR PUI SUSANNA

APPLICANT: HOON, LIT MAN

APPLICANT: POON, LIT MAN

APPLICANT: POON, LIT MAN

TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT

TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT

TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING

FILE REFERENCE: V6690.0044

CURRENT PILING DATE: 2006-05-16

PRIOR FILING DATE: 2004-07-21

NUMBER OF SEQ ID NOS: 4257

SEQ ID NO 2685

LEBOTH: SAME PATRICALLY VERSION 3.3

LEBOTH: SAME PATRICALLY VERSION 3.3

LEBOTH: SAME PATRICALLY VERSION 3.3

LEBOTH: SAME PATRICALLY VERSION 3.3
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Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels
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100.0%; Score 10; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels
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CORGANISM: Corononavirus-HKU1
US-11-129-741-2685
    ; SEQ ID NO 365
; LENGTH: 5
; TYPE: PR: 7
; ORGANISM: Homo sapiens
US-11-145-861-365
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HITLE OF INVENTION: UNIQUE RECCGNITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVENTION: UNIQUE RECCGNITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVENTION: UNIQUE RECCGNITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVENTION: UNIQUES: 10/436,549

PRIOR PELICATION NUMBER: 10/436,549

PRIOR PELICATION NUMBER: 60/379,626

PRIOR PELICATION NUMBER: 60/393,137

PRIOR PELICATION NUMBER: 60/393,137

PRIOR PELICATION NUMBER: 60/393,217

PRIOR PELICATION NUMBER: 60/393,217

PRIOR PELICATION NUMBER: 60/393,217

PRIOR PELICATION NUMBER: 60/393,217

PRIOR PELICATION NUMBER: 60/393,233

PRIOR PELICATION NUMBER: 60/393,233

PRIOR PELICATION NUMBER: 60/393,233

PRIOR PELICATION NUMBER: 60/393,235

PRIOR PELICATION NUMBER: 60/393,235

PRIOR PELICATION NUMBER: 60/393,235

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PRIOR PELICATION NUMBER: 60/3
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Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels
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ORGANISM: Homo sapiens
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APPLICANT: Lee, Frank D.
APPLICANT: Lee, Frank D.
APPLICANT: Chan, John W.
APPLICANT: Chang, Shengsheng
APPLICANT: Chang, Shengsheng J.
APPLICANT: Chang, Shengsheng J.
TITLE OF INVERTION: UNIQUE RECCRITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVERTION: UNIQUE RECCRITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVERTION: UNIQUE RECCRITION SPECIAL SETTION SPECIAL SPECIAL SETTION SPECIAL SPECIAL SETTION SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL S
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Publication No. US20060035270A1
PEDREAL INCORMATION:
APPLICANT: Lee, Frank D.
APPLICANT: Meng, Dr. Xun
APPLICANT: Chan, John W.
APPLICANT: Chan, John W.
APPLICANT: Zhang, Shengsheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 491, Application US/11249847
Publication No. US20060035270A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 2; Conservative
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CORGANISM: Homo sapiens
US-11-249-847-491
                                                                                      Query Match
Best Local Similarity
Matches 2; Conserv
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US-11-249-847-493
US-11-249-847-486
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Tue Feb 28 11:30:39 2006

5.1.7	Biocceleration Ltd.
version	- 2006
GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

February 28, 2006, 08:45:35 ; Search time 0.121972 Seconds
(without alignments)
1577.691 Million cell updates/sec

Run on:

US-10-717-665A-44_COPY_448_449 10 Title: Perfect score:

1 RM 2 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters: 283416. Minimum DB seq length: 0

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ф			SOMESTIES	
Result No.	Score	Query Match	Length	DB		Description
	10	100.0	1 1 1 1	2	PT0298	Ig heavy chain CRD
7	10	100.0	σ	~	PT0670	T-cell receptor be
٣	10	100.0	Н	7	PC4442	cytochrome c553 -
4	10	100.0	11	~	E60691	phycobilisome 8K l
S	10	100.0	12	7	A42324	cytochrome P450c27
9	10	100.0	12	7	T44420	1 prot
7	10	100.0	14	7	PC1215	
80	10	100.0	14	7	H83778	
σ	10	100.0	15	7	A56786	pimeloyl-CoA synth
10	10	100.0	15	~	PA0020	protein QA100028 -
11	10	100.0	15	~	A45096	thyrotropin-releas
12	10	100.0	16	N	S24667	protein-tyrosine k
13	10	100.0	16	N	S11805	heat shock protein
14	10	100.0	16	~	A41170	Ψ
15	10	100.0	16	7	S78415	ribosomal protein
16	10	100.0	16	~	E37290	
17	10	100.0	17	~	A34835	ribosomal protein
18	10	100.0	17	~	S77834	DNA-directed RNA p
19	10	100.0	18	N	B24735	
20	10	100.0	-	~	S32548	glutathione transf
21	10	100.0	7	N	S31613	beta-1,3-glucanase
22	10	100.0	20	N	829100	glutathione transf
23	10	100.0	20	~	S30381	ħ
24	10	100.0	7	N	E60894	crystallin - Pacif
25	10	100.0	7	N	A44773	pollen allergen I
26	10	100.0	7	~	PC4385	GroEL protein homo
27	10	100.0	20	~	œ	
28	10	100.0	20	~	E54226	light-harvesting p
59	10	100.0	20	0	A56899	serum heterodimer,

10 100.0	
10 100.0 22 2 B58793	
10 100.0 23 2 H24735	
10 100.0 23 2 148936 cryptdin	
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10 100.0 24 2 \$30373	
10 100.0 24 2 T42441 protein phosphat	
10 100.0 24 2 A33262 heparin-binding	
10 100.0 24 2 H53578	
10 100.0 24 2 T07991	
ALIGNMENTS	
RESULT 1	
190250 Ighavy chain CRD3 region (clone 5-103A) - human (fragment)	
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996	
C;Accession: PT0298	
RiYamada; M.; Wasserman, K.; Kelchard, B.A.; Shane, S.; Caton, A.J.; Kovera, G. I Tevn Mad 173 195-407 1991	
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and	ı jc
A; Reference number: PT0222; WUID:91108337; PMID:1899102	
A;Accession: PT0298	
A Molecule type: DNA	
A) WESTGLES I - O SILMY A CHASSIGNES I TO SILMY STATEMENT TO THE STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATE	
A:Cobs.terimics: OnIncor: A:Experimental Gource: B lymphocyte	
C; Keywords: heterotetramer; immunoglobulin	
100.0%; Score 10;	
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Marches 2: Conservative 0: Mismatches 0: Indels 0: Gads 0;	

T-cell receptor beta chain V-D-J region (121-1BN) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0670
R;Peeney, A.J.
J; Exp. Med: 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Accession: PT0670
A;Accession PT0670
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A;Accession pr0670
A;Accession profer
A;Molecule type: mRNA
A;Residues: 1-9 <FRE>
A;Residues: 1-9 <FRE>
A;Residues: 1-9 <FRE>
A;Residues: 1-9 <FRE>
A;Experimental source: day 4 postnatal thymus, strain BALB/C
C;Keywords: T-cell receptor .; 0 Gape .. 0 .. o Mismatches ; 0 2; Conservative 1 RM 2 1 RM 2 Matches RESULT 2 PT0670 셤 Š

Gaps ö Query Match
100.0%; Score 10; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels

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hypothetical protein BH1032 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Dacession: H83778
C;Accession: H83778
R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and SA;Reference number: A83650; MUD:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homeotic protein EgHbx5 - tapeworm (Echinococcus granulosus) (fragment)

C;Species: Echinococcus granulosus
C;Species: Bchinococcus granulosus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: PC1215
R;Oliver, G; Vispo, M; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlich
Gene 121, 337-342, 1992
A;Title: Homeoboxes in flatworms.
A;Reference number: JC1386; MUID:93077050; PMID:1359988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CiAccession: T44420
R;Vlaskova, H.; Krasny, L.; Fucik, V.; Jonak, J.
Submitted to the EMBL Data Library, September 1997
Submitted to the EMBL Data Library, September 1997
Submitted to the EMBL Data Library, September 1997
Submitted to the EMBL Data Library, September 1997
A;Reference number: Z22760
A;Reference number: Z22760
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A;Experimental source: strain CCM 2184
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein [imported] - Bacillus stearothermophilus (fragment) C;Species: Bacillus stearothermophilus C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels
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100.0%; Score 10; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 2; Conservative 0; Mismatches 0; Indels
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A;Residues: 1-14 <OLI>
A;Cross-references: UNIPARC:UPI000017B68F; EMBL:X66821
C;Keywords: homeobox
100.0%; Pred. No. 9.1e+02; ive 0; Mismatches 0;
          Best Local Similarity 100.
Matches 2; Conservative
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A;Status: preliminary
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J. Biol. Chem. 267, 2421-2428, 1992
A;Title: Sequence complementarity between the 5'-terminal regions of mRNAs for rat mitod
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A;Molecule type: 1-11 <BRY>
A;Cross-references: UNIPARC:UPI000017ABC5
C;Comment: This protein, one of the eleven components detected in this species of the ph
C;Keywords: photosystem II
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Bhycobilisome 8K linker protein - Synechococcus sp. (PCC 7002) (fragment)

C;Species: Synechococcus sp.

C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999

C;Accession: E60691

R;Bryant, D.A.; de Lorimier, R.; Guglielmi, G.; Stevens Jr., S.E.

Arch. Microbiol. 153, 550-560, 1990

A;Title: Structural and compositional analyses of the phycobilisomes of Synechococcus
                                                                                                                                                           Cytochrome c553 - Desulfovibrio desulfuricans (fragment)
Cybecies: Desulfovibrio desulfuricans
Cybecies: Desulfovibrio desulfuricans
C;Date: 28-Mar-1998 #sequence_revision 28-Mar-1998 #text_change 09-Jul-2004
C;Date: 28-Mar-1999 #sequence_revision 28-Mar-1998 #text_change 09-Jul-2004
C;Accession: PC4442
B;Aubert, C.; Leroy, G.; Bianco, P.; Forest, E.; Bruschi, M.; Dolla, A.
B;Arbert, C.; Leroy, G.; Bianco, P.; Forest, E.; Bruschi, M.; Dolla, A.
B;Arbert, C.; Leroy, G.; Bianco, P.; Forest, E.; Bruschi, M.; Dolla, A.
B;Arbertence number: PC4442
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: -10 < AUBR-A
A;Cossion: PC4442
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Feb-1996
C;Accession: A42324
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 < SHA>
A;Cross-references: UNIPARC:UPI000017C8FA
A;Note: sequence extracted from NCBI backbone (NCBIN:78404, NCBIP:78410)
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Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 2; Conservative 0; Mismatches 0;
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Best Local Similarity 100. Matches 2; Conservative

Query Match

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100.0%; Score 10; DB 2; Length 14; 100.0%; Pred. No. 1e+03;

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thyrotropin-releasing hormone receptor, splice form 387 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A45096
R;de la Pena, P.; Delgado, L.M.; del Camino, D.; Barros, F.
J. Balol. Chem. 267, 25703-23708, 1992
A;Title: Two isoforms of the thyrotropin-releasing hormone receptor generated by alternat A;Reference number: A45096
A;Accession: A45096
A;Accession: A45096
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-15 < DEL>
A;Cross-references: UNIPARC:UPI0000170C44; GB:S51512; NID:g261982; PIDN:AAB24549.1; PID:gA;Reperimental source: GH3 anterior pituitary cells
A;Rote: sequence extracted from NCBI backbone (NCBIP:120927)
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S24667
R;Sorrentino, V.
Submitted to the EMBL Data Library, May 1992
A;Reference number: S24666
A;Accession: S24667
A;Accession: S24667
A;Accession: S24667
A;Return: preliminary
A;Molecule type: DNA
A;Residus: 1-16 <SONA
A;Residus: 1-16 <SONA
A;Residus: 1-16 <SONA
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
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C;Species: Comamonas acidovorans
C;Species: Comamonas acidovorans
C;Accession: S11805; S22676
R;Hallett, P.; Mehlert, A.; Maxwell, A.
Mol. Microbiol. 4, 345-353, 1990
A;Title: Escherichia coli cells resistant to the DNA gyrase inhibitor, ciprofloxacin, ove A;Reference number: S11805; MuID:90286912; PMID:1972534
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A;Residues: 1-16 cHAL>
A;Cross-references: UNIPROT:Q9R5K5; UNIPARC:UPI000017A951
A;Note: the species identification has been revised in reference 822676
R;Fowell, S.L.; Lilley, K.S.; Jones, D.; Maxwell, A.
Mol. Microbiol: 6, 1575-1576, 1992
A;Title: GroEL proteins from three Pseudomonas species.
A;Reference number: S22676; MUID:92126641; PMID:1352616
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100.0%; Score 10; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels
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C.Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C.Accession: PA0020
R.Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A.Description: Separation and characterization of Arabidopsis proteins by two-dimensiona
                                                                                    A;Cross-references: UNIPROT:Q9KE26; UNIPARC:UP100000C3A89; GB:AP001510; GB:BA000004; NID A;Experimental source: strain C-125 C;Genetics: A;Gene: BH1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C)Accession: A56786
R)Ploux, O.; Soularue, P.; Marquet, A.; Gloeckler, R.; Lemoine, Y.
Biochem. J. 287, 685-690, 1992
A;Title: Investigation of the first step of biotin biosynthesis in Bacillus sphaericus. A;Reference number: A56786; MUID:93075017; PMID:1445232
A;Accession: A56786
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A;Retsidus: preliminary
A;Molecule type: protein
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A,Note: sequence extracted from NCBI backbone (NCBIP:117639)
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C;Species: Bacillus sphaericus
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Aug-1995
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Query Match 100.0%; Score 10; DB 2; Length 15; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 2; Conservative 0; Mismatches 0; Indels

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A;Gene: bioW C;Keywords: biotin biosynthesis; homodimer

C; Genetics:

A; Cross-references: UNIPARC: UPI000017ACA8

protein QA100028 - Arabidopsis thaliana (fragment)

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Query Match
100.0%; Score 10; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels

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ઠે 유 RESULT 11 A45096

A;Molecule type: protein A;Residues: 1-15 <KRAM> A;Cross-references: UNIPARC:UPI000017AFE7 A;Experimental source: callus

A; Reference number: PA0001 A; Accession: PA0020

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RESULT 14

441170

photosystem II 6.1K protein - Chlamydomonas reinhardtii (fragment)

c;Species: Chlamydomonas reinhardtii

c;Species: Chlamydomonas reinhardtii

c;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004

c;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004

R;de Vitry, C.; Diner, B.A.; Popot, J.L.

J. Biol. Chem. 266, 16614-16621, 1991

A;Title: Photosystem II particles from Chlamydomonas reinhardtii. Purification, molecula A;Reference number: A41170; MUID:91358452; PMID:1885590
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100.0%; Score 10; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels
A;Note: the source is designated as Pseudomonas acidovorans C;Genetics:
A;Gene: groEL
C;Keywords: molecular chaperone
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A;Molecule type: protein
A;Residues: 1-16 < DEV.
A;Cross-references: UNIPROT:Q7MlJ4; UNIPARC:UPI000017AF05
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Q4y54 plasmodium
Q5ia44 philodendro
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae; Laurus.
NCBI_TaxID=85223;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Proc. Natl. Acad. Sci. U.S.A. 101:17747-17752(2004)
EMBL; AY892169; AAW11502.1; -; Genomic_DNA.
GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                     8 AA.
 044W45_FUGRU
09AXW9_BRADL
09AXW2_BRADL
09AXW2_BRANA
07M14_GHLRE
07M0C9_RAT
07M0C9_RAT
07M0C9_RAT
07M0C9_RAT
07M0C9_RAT
07M0C9_LEAM
07MX3_LEIME
04XM10_FUAN
05UW77_9LAMI
05UW77_9LAMI
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10-WAY-2005 (TrEMBLrel. 30, Last annota
NADH dehydrogenase subunit 4 (Fragment)
Namesnad4;
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Homo sapiens (Human).
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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QSIA47;
10-MAY-2005 (TYEMBLYEL: 30,
10-MAY-2005 (TYEMBLYEL: 30,
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QOUKJE;
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  NCBI_TaxID=9606;
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Q9UKJ6_HUMAN
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NUCLEOTIDE SEQUENCE. Zhang W., Li X.Q., Wu Q.F.;

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"Massive horizontal transfer of mitochondrial genes from diverse land plant donors to the basal angiosperm Amborella."; Proc. Natl. Acad. Sci. U.S.A. 101:17747-17752(2004). EMBL; AY832171; AAW31504.1; -; Genomic_DNA.
                                                       Palmer J.D.;

"Massive horizontal transfer of mitochondrial genes from diverse land plant donors to the basal angiosperm Amborella.";

Proc. Natl. Acad. Sci. U.S.A. 101:17747-17752 (2004).

EMBL; AX832172; AAW31505.1; -; Genomic_DNA.

GO; GO:0005739; C:mitochondrion; IEA.

Mitochondrion.

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NA, 996 MW; D35B7772C8768412 CRC64;
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Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Berberidaceae; Mahonia.
NCBI_TaxID=13601;
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PubMed=15598737; DOI=10.1073/pnas.0408336102;
Bergthorsson U., Richardson A.O., Young G.J., Goertzen L.R.,
NUCLEOTIDE SEQUENCE.
PubMed=15598737; DOI=10.1073/pnas.0408336102;
Bergthorsson U., Richardson A.O., Young G.J., Goertzen L.R.,
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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10-MAY-2005 (TrEMBLrel. 30, Last annota
10-MAY-2005 (TrEMBLrel. 30, Last annota
NADH dehydrogenase subunit 4 (Fragment)
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Q7MOM6;
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QSIA45;
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Matches 2; Conservative
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nes 2; Conservative
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Hall N., Karras M., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafātos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
"A comprehensive survey of the Plasmodium life cycle by genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; Liliopsida, Araceae, Aroideae, Philodendreae, Philodendreae, Philodendron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                             h Similarity 100.0%; Score 10; DB 2; Length 9; Similarity 100.0%; Pred. No. 2.2e+06; 2; Conservative 0; Mismatches 0; Indels
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  Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIS9087; AAF04001.1; -; Genomic_DNA.
GO; GO:0004872; F:receptor activity; IEA.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
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SEQÜENCE 9 AA; 1272 MW; 6F2B8415B331E684 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.

EMBL; CAAJ01000035; CAH74304.1; -; Genomic_DNA.

Hypothetical protein.
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OSIA44 9ARAE

ID Q5IA44 9ARAE PRELIMINARY;

DT 10-MAY-2005 (TrEMBLrel. 30,

DT 10-MAY-2005 (TrEMBLrel. 30,

DT 10-MAY-2005 (TrEMBLrel. 30,

DT 10-MAY-2005 (TrEMBLrel. 30,

DE NADH dehydrogenase subunit 4

GN Name=nad4;

OS Philodendron oxycardium.

OG Mitochondrion.

OK Nitochondrion.

OK Spermatophyta; Magnoliophyte

OC Philodendreae; Philodendron.

OX NOBI TAXID=71614;
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Q4Y954 PLACH PRELIMINARY;
Q4Y954;
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Best Local Similarity
Matches 2: Conserv
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Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio.

Cytochrome c553 (Fragment). Desulfovibrio desulfuricans.

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revealed in the avian genome.";
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QBJJ33;
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ID Q709BO_HUMAN PRELIMINARY;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92174914; PubMed=1541289;
Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;
"Molecular characterization of six intermediate proteins in the
processing of mouse protaine P2 precursor.";
Eur. J Biochem. 204:759-765(1992)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
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Primmer C.R., Barge T., Lindell J., Saetre G.P.;
"Single-nucleotide polymorphism characterization in species with
limited available sequence information: high nucleotide diversity
                                                       MEDITAL SECTION 1997.7852; MEDITAL SECTION OF ADDRESSION OF AUBERT C., Lercy G., Bianco P., Forest E., Bruschi M., Dolla A.; "Characterization of the cytochromes C from Desulfovibrio desulfuricans G201.";
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                                                                                                                                              Biochem. Biophys. Res. Commun. 242:213-218(1998).
PIR; PC4442; PC4442.
NON TER 10 10 SEQÜENCE 10 AA; 1112 MW; 87C51E5735BDD87A CRC64;
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SEQÜENCE 10 AA; 1280 MW; 01DD2975A406841B CRC64;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Last sequ
01-FEB-2005 (TrEMBLrel. 29, Last anno
Myelin proteolipid protein (Fragment)
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Q9QVP1_9MURI PRELIMINARY;
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QGJFE7 FICAL PRELIMINARY;
QBJFE7;
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Best Local Similarity
Matches 2; Conserv
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                                       PROTEIN SEQUENCE
NCBI_TaxID=876;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
NCBI_TaxID=46689;
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Kuiper R.P., Schepens M., Thijssen J., Schoenmakers B.F.P.M.,
Geurts van Kessel A. "Regel A." "Regelation of the MITF/TFE bHLM-LZ transcription factors through
"Regulation of the MITF/TFE bHLM-LZ transcription factors through restricted spatial expression and alternative splicing of functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE=21918460, PubMed=11918793;
MEDLINE=21918460, PubMed=11918793;
Primmer C.R., Borge T., Lindell J., Saetre G.P.;
Mingle-nucleotide polymorphism characterization in species with
"Single-nucleotide polymorphism characterization in species with
"Inmited available sequence information: high nucleotide diversity
revealed in the avian genome.";
Mol. Ecol. 11:603-612(7002).
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                                                                                                                                                                                                                                             Length 10;
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10 AA; 1206 MW; 1FAAC9676732C86B CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Myelin proteolipid protein (Fragment).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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100.0%; Pred. No. 3.8e+03;
ative 0; Mismatches 0;
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MO1. Ecol. 11:603-612(2002).
EMBL; AF454217; AAM22903.1; -; Genomic DNA.
EMBL; AF454218; AAM22904.1; -; Genomic DNA.
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Gaps

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Length 12; Indels

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NON TER 1 1
NON TER 12 12
SEQÜENCE 12 AA; 1442 MW; 7500ECB95A172684 CRC64;
                                                                         100.0%; Score 10; DB 2; I
100.0%; Pred. No. 4.6e+03;
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050303;
                                                          Query Match
Best Local Similarity luv..
2; Conservative
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P95606_ALCEU PRELIMINARY;
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Best Local S:
Matches 2
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BMBL; AF229414; AAK00686.1; -; Genomic DNA.
GO; GO:0008020; F:G-protein coupled photoreceptor activity; IEA.
GO; GO:0009585; P:red, far-red light phototransduction; IEA.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                 100.0%; Score 10; DB 2; Length 11; 100.0%; Pred. No. 4.2e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2005); -; Genomic_DNA. NON TER 12 12 12
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                                                                                                          11 AA; 1276 MW; 7BB98CBD07287044 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Transcription factor EB (Fragment).
Name=TFEB; ORFNames=RP4-696P19.3-012;
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      Nucleic Acids Res. 32:2315-2322 (2004).
EMBL; AJ608782; CAE77674.1; -; mRNA.
EMBL; AJ608782; CAE77677.1; -; mRNA.
BMBL; AJ608788; CAE77673.1; -; mRNA.
NON TER
11 11
SEQÜENCE 11 AA; 1276 MW; 7BB98GEDD
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Name=BN-PHYA-2;
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Matches 2; Conservative
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Best Local Similarity 100.
Matches 2; Conservative
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Q4VXX2_HUN
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MEDLINE=20194845; PubMed=10732707;
MEDLINE=20194845; PubMed=10732707;
Vlaskova H., Krasny L., Fucik V., Jonak J.;
"The pyrab gene coding for the large subunit of carbamoylphosphate synthetase from Bacillus stearchermophilus: molecular cloning and functional characterization.";
Polia Biol. (Praha) 44:163-172(1998).
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                                                                                                                                                                                                                Alcaligenes eutrophus (Ralstonia eutropha).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Cupriavidus.
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
NCBL_TaxID=1422;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                     01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Nickel permease (Fragment).
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12 AA.
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NOW_TER 12
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Q9TQS4 HORSE

ID Q9TQS4 HORSE PRELIMINARY; PRT; 13 AA.

AC Q9TQS4,

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-PEB-2005 (TrEMBLrel. 29, Last annotation update)

DT 1-PEB-2005 (TrEMBLrel. 29, Last annotation update)

E Transferrin (Fragment).

DE Transferrin (Fragment).

C Educ caballus (Horse).

C Educ caballus (Horse).

C Educ caballus (Horse).

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C C NCBL Entheria; Laurasiatheria; Perissodactyla; Equidae; Equus.

C NCBL TAXID-9796;
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Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                Ouery Match 100.0%; Score 10; DB 2; Length 12; Best Local Similarity 100.0%; Pred. No. 4.6e+03; Matches 2; Conservative 0; Mismatches 0; Indels
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Giffard J.M., Brandon R.B., Bell T.K.;
Submitted (SEP-199) to the EMBL/GenBank/DDBJ databases.

EMBL; AF185755; AAF05469.1; -; Genomic_DNA.

EMBL; AF185754; AAF05468.1; -; Genomic_DNA.

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SEQUENCE 13 AA; 1528 MW; D379D35F2EA2840D CRC64;
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	GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceles	5.1.7 Biocceleration Ltd.
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	US-10-717-665A-44_COPY_532_639	
Periect score: Sequence:	551 1 KLAFRACRIKKKAQYEANKVTAEGNPTGGLVGLRIPTSKV 108	TGGLVGLRIPTSKV 108
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	
Searched:	2443163 segs, 439378781 residues	-
Total number of	Total number of hits satisfying chosen parameters:	2443163
Minimum DB seq 1 Maximum DB seq 1	Minimum DB seq length: 0 Maximum DB seq length: 200000000	
Post-processing:	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database :	A_Geneseq_21:* 1:geneseqp1980s:* 2:geneseqp1980s:* 3:geneseqp2000s:* 4:geneseqp2001s:* 6:geneseqp2001s:* 7:geneseqp2003as:* 7:geneseqp2003bs:* 8:geneseqp2003bs:* 9:geneseqp2005s:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Adk65805 Angiogene	Ado20373 Human PRO	4	Abg29275 Novel hum	Abull886 Human ABC	Abu19277 Protein e	Abu01541 S. pneumo	_	Ads44237 Bacterial	Ads30935 Bacterial	Abu43663 Protein e	Ads30054 Bacterial		'n	Abu61812 Human nuc	Adg86291 Human SMR	Adq18921 Human sof	Ads88212 Human pro	Abm85413 Human pro	Adg86299 Human SMR	₩.	Aab48935 Brassica	Adk47294 Streptoco	Adr94210 Novel S.
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ΩΙ	ADK65805	AD020373	ABB68374	ABG29275	ABU11886	ABU19277	ABU01541	ADM92163	ADS44237	ADS30935	ABU43663	ADS30054	AAW18226	ADN04305	ABU61812	ADG86291	ADQ18921	ADS88212	ABM85413	ADG86299	AAB40574	AAB48935	ADK47294	ADR94210
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Length	639	296	814	160	1124	281	345	642	1175	1124	625	1104	1495	2000	2507	2507	2507	2514	2517	2517	2518	510	642	651
% Query Match	100.0	98.5	36.7	36.4	14.9	14.2	13.7	13.7	13.7	13.5	13.3	13.3	13.3	13.3	13.3	13.3	13.3	13.3	13.3	13.3	13.3	13.2	13.2	13.2
Score	551	543	202	200.5	82	78.5	75.5	75.5	75.5	74.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	72.5	72.5	72.5
Result No.	H	N	e	4	ហ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Aea58080 Streptoco	Adn20856 Bacterial	Abb65505 Drosophil	Adn26279 Bacterial	Adn22598 Bacterial	Adn22599 Bacterial		Aag67384 Amino aci		Adv16175 X. pelarg	Aag67386 Amino aci	Adn20163 Bacterial	Ady86677 Human GRP	Ady86676 Human GRP		Adn99816 Novel hum	Adf77333 Heat shoc	Aae23607 Human end	Abp26389 Streptoco	Abu46647 Protein e	Adn99815 Novel hum
AEA58080	ADN20856	ABB65505	ADN26279	ADN22598	ADN22599	ADK64278	AAG67384	ADN20612	ADV16175	AAG67386	ADN20163	ADY86677	ADY86676	ADN72115	ADN99816	ADF77333	AAE23607	ABP26389	ABU46647	ADN99815
6	œ	4	80	8	œ	7	4	ω	α	4	œ	6	6	œ	œ	ß	S	S	9	8
651	861	505	825	1355	1355	667	487	597	640	846	1105	152	188	190	194	220	223	282	282	287
13.2	13.1	12.9	12.9	12.9	12.9						12.6	12.5	12.5	12.5	12.5	12.5	12.5	12.5	12.5	12.5
72.5	72	71	71	71	71	70.5	70	70	70	70	69.5	69	69	69	69	69	69	69	69	69
25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

cytostatic; cardiant; vasotropic; antiarteriosclerotic; angiogenesis inhibitor; angiogenesis stimulator; angiogenesis stimulator; angiogenes; gene expression; cancer; coronary artery disease; myocardial ischemia; coronary arteriosclerosis; forensic medicine. Angiogenesis-differentially expressed protein ANH0757. ADK65805 standard; protein; 639 AA. (first entry) 06-MAY-2004 ADK65805; ADK65805 

Ното варіепв

WO2003066831-A2.

14-AUG-2003.

07-FEB-2003; 2003WO-US003848.

07-FEB-2002; 2002US-00067482. 10-JUN-2002; 2002US-00164595. 16-AUG-2002; 2002US-0403649P. 03-JAN-2003; 2003US-0437746P.

(ORIG-) ORIGENE TECHNOLOGIES INC

Jay G;

Li X, Kovacs KF, Fan W,

Sun Z,

WPI; 2003-731502/69. N-PSDB; ADK65804.

Determining the angiogenic index of a tissue or cell sample using expression levels of differentially expressed genes, useful for diagnosing or treating cancer, coronary artery disease, myocardial ischemia and/or arteriosclerosis.

Claim 23; SEQ ID NO 44; 296pp; English.

The invention relates to a method of determining the angiogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the angiogenic index. The methods and compositions of the present

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                                                                                                                                                                                                                                          532 KLAFRACRIKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ 591
                                                                                                                                                                                                            09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Gulllain-Barre syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human PRO polypeptides and the polymucleotides encoding them. The polypeptides and polymucleotides are useful for treating and diagnoshig immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, artoridusis, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the
invention are useful for diagnosing, preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary arteriosclerosis. They can also be used in research, drug discovery and forensic medicine involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention.
                                                                                                                                                                                                        1 KLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ
                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                   KLEILIKDTLGLPVAGQISEFVNQVLEKTAEGNPIGGLVGLRIPISKV 108
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chronic inflammatory demyelinating polyneuropathy.
                                                                                                                                                                               ö
                                                                                                                                         100.0%; Score 551; DB 7; 100.0%; Pred. No. 1.1e-53;
                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                         ADO20373 standard; protein; 296 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2003; 2003WO-US035268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-2002; 2002US-0425235P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO polypeptide #633
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                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-420067/39.
N-PSDB; ADO20372.
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                                                                                                                                                             Similarity
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                                                                                                           Sequence 639 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                             Query Match
Best Local Simil
Matches 108; C
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WI,
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                                                                                                                                                             Best Local
Matches
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Wood
                                                                                                                                                                                                                                                                                                                                                                                           ADO20373
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                                                                                                                                                 ö
                                                                                                                                                                                                              189 KLASRACRLKKKRAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNWGQ 248
                                                                                                                                                                                9
central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                1 KLAFRACKLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ
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                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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                                                                                                                                                                                                                                                61 KLEILIKUTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 108
                                                                                                                                                                                                                                                                     249 KLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 296
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Local Similarity 43.6%; Pred. No. 1e-13;
es 48; Conservative 17; Mismatches 31; Indels 1
                                                                                                                    Length 296;
                                                                                                                98.5%; Score 543; DB 8; Length 29
99.1%; Pred. No. 3.5e-53;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 31914.
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                                                                                                                                                                                                                                                                                                                                                                        AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                     Best Local Similarity 99.1
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
N-PSDB; ABL12477.
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                                                                                      Sequence 296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving aberrant procein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                         708 KLASRACRLKKKAQHEANKIKLPGLEIEHKRLMNGIAEJKQALVVK-----HRTKNLGE 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
1 KLAFRACRLKKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forensic;
                                                                                                                                               102
                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                               61 KLE-----ILIKDILGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #29266.
                                                                                                                                                                                                                                                                                                                                                                                                     ABG29275 standard; protein; 160 AA
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23-AUG-2000; 2000US-00649167
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The present invention relates to high throughput screening assays for agents capable of modulating the activity of ATP-binding cassette transporter I (ABCA1, also called cholesterol efflux regulating protein (CERP)). The method comprises determining the activity of an ABCA1 polypeptide in the presence of an ABCA1-interacting protein (AIP) that polypeptide in the presence of an ABCA1-interacting protein (AIP) that has been contacted with an agent. The method is useful for identifying agents that modulate cholesterol or phospholipid levels in an animal. The method is useful for treating disorders of lipid metabolism, especially for reducing elevated plasma phospholipid or cholesterol levels in a patient at risk of developing disorders such as cardiovascular in a patient at risk of developing disorders such as cardiovascular clisease (CMD), coronary aretery disease (CMD), cerebrovascular disease, coronary restenosis, and peripheral vascular disease. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying ABCA1 (cholesterol efflux regulating protein) modulators for modulating cholesterol or phospholipid levels in animals, by determining ABCA1 activity in the presence of an agent-contacted ABCA1-interacting
                                                                 9 LKKKKAQYEANKVKLW-GLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIK 67
                                                                                      High throughput screening assay; ATP-binding cassette transporter 1; ABCA1; cholesterol efflux regulating protein; CBRP; AIP; human; ABCA1-interacting protein; plasma cholesterol; plasma phospholipid; lipid metabolism disorder; cardiovascular disease; CVD; CAD; coronary artery disease; cerebrovascular disease; coronary restenosis;
                                  Gaps
                                  .,
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                                  Indels
Pred. No. 1.9e-14;
                                                                                                                                                                                                                                                                                                                                                                Human ABCA1 interacting polypeptide KIAA0528.
                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peripheral vascular disease; anti-lipaemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 59-63; 92pp; English
                                                                                                                                                                                                                                                               ABU11886 standard; protein; 1124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Newman SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XENON GENETICS INC.
UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2002; 2002WO-CA000489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-2001; 2001US-0283424P.
                  73.0%;
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                    46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang L, Hayden MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-093046/08
                  Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABX55992
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                                                                                                                                         68 DIL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200284301-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                               ABU11886;
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14.9%; Score 82; DB 6; Length 1124;

Query Match

Length 160;

DB 4;

36.4%; Score 200.5;

Query Match

identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, R. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

6; Length 281;

DB

ftp.wipo.int/pub/published_pct_sequences

888888888888888

Sequence 281 AA;

Query Match

proliferation of an organism. The antisense nucleic acids are useful for

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are: of the mucleic acid inhibits proliferation of a cell. Also included are: cocding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated or polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid, (4) an antibody capable of specifically binding cate polypeptide (5) producing the polypeptide; (6) inhibiting cellular consoliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway creduired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological control pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture computation in which the est compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture computation in which the extent compound; such activity; (11) a culture organism acts; (12) determining the extent compount that inhibits proliferation of the strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                  9
                                                                                            590 RICKLKKKAQAEANA-----TAISNLLPFMEYEVHTQLMNKLK----LKGMNALFGLR 638
                                                     5 RACRIKKKAQYEANKVKIMGINTEYDNIL-FVINSIKQEIVNRVQNPRDERGPN--MGQK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind JW;
Xu HH;
                    Gaps
                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohlsen KL,
Forsyth RA,
                      27; Indels
                                                                                                                                                               62 LEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #4804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck R,
Yamamoto R,
28.4%; Pred. No. 7.5; tive 22; Mismatches
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                                                                                                                                                                                                                                                                                  ABU19277 standard; protein; 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2002; 2002WO-US009107.
      Best Local Similarity 28.4%, Matches 29, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi
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Wall D,
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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable formath), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a
                                                      72
                                                                                                                                                                                                                                                                                                                                                      Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media cear infection.
                                                                        21 KIMGLNTEYDNLLFVIN-SIKQEIVNRVQNPRDER----GPNMGQKLEILIKDT---LGL
                            23; Indels 15;
                                                                                                                                                                                                                                                                                                                                S. pneumoniae type 4 strain protein from coding region #1117.
14.2%; Score 78.5; Dl
31.6%; Pred. No. 3.2;
                             14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae; type 4 strain.
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                                                                                                                                                                                                                             ABU01541 standard; protein; 345 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2002; 2002WO-IB002163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2001; 2001GB-00007658.
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84 EIDLKYSEILNEKFGK 99
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                                                                                                                        73 PVAGQTSEFVNOVLEK
                                24; Conservative
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N-PSDB; ABX06829.
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                 Similarity
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                                                                                                                                                                                                                                                                                                          11-FEB-2003
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                       Local
                                  Matches
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composition, and cited above or fragments between nuclectides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where sequence contained within a Streptococcus nucleic acid sequence.

The first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having substantial complementarity define the termin of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, media or ear infection. They are also useful in developing vaccines, immunodominant proteins. The methods are useful for identifying immunodominant proteins. The methods are useful for identifying cimmunodominant proteins. The methods are useful for identifying immunodominant proteins requence is one of the 2469 proteins expressed by the identified coding regions from the genomic sequence.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Earddardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LKKKAQYEANKVK-----LWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM-- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus pneumoniae nucleic acid molecules, useful for diagnosing, treating and preventing active infections of Streptococcus pneumoniae.
composition), a kit comprising first and second primers, which are the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial; gene therapy; Streptococcus pneumoniae infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 13.7%; Score 75.5; DB 6; Length 345; Local Similarity 27.6%; Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GOKLEILI------KD-TLGLPVAGQTSEFVNQVLEK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S pneumoniae antigenic protein sequence SeqID360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-SEP-2003; 2003WO-US027401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2002; 2002US-0407082P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-239189/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 345 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigenic
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                          This invention relates to novel isolated Streptococcus pneumoniae nucleic acid molecules and the antigenic polypeptides encoded by them. The invention may be useful for the production of compounds with an antibacterial activity or for gene therapy. The nucleic acid molecules, compositions and methods disclosed are useful for treating Streptococcus pneumoniae infection. The present sequence is that of an S pneumoniae protein of the invention.
                                                                                                                                                                                                                                                                     The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cold tolerance, heat tolerance, drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant DNA construct; transformed plant; improved plant property;
                                                                                                                                                                                                                                                    9 LKKKAQYEANKVK-----LWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM--
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                       39;
                                                                                                                                                                                        DB 8; Length 642;
                                                                                                                                                                                                                                                                                                                                   20; Indels
                                                                                                                                                                                                                                                                                                                 59 ----GQKLBILI-----KD-TLGLPVAGQTSEFVNQVLEK 88
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                                                                                                                                                                                                                     17; Mismatches
                                                                                                                                                                                        Score 75.5; |
Pred. No. 20;
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Claim 27; SEQ ID NO 360; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADS44237 standard; protein; 1175 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial polypeptide #22667.
                                                                                                                                                                                        13.7%;
27.6%;
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                                                                                                                                                                       Query Match
Guery Cocal Similarity 27.00.
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GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HINKLE G J.
SLATER S C.
                                                                                                                                                        Sequence 642 AA;
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(CHEN/)
(GOLD/)
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(HINK/)
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                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
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c comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant combinant an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. Improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of catbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and continged to the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of 
                                                                                                                                                                                                                                                                                                                                                                                                                       production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 VCLNSCRFYNETRSQLREKRFFVGXNLYINILFLISNVKRIRASRNQDNRPERQSRL-QR 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.7%; Score 75.5; DB 8; Length 1
25.0%; Pred. No. 44;
.ive 21; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 SSSLIEQVRG-----NEDGENDVLNOTRETN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 LEILIKDTLGLPVAGOTSEFVNOVLEKTAEGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADS30935 standard; protein; 1124 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial polypeptide #19968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 25.0% les 23; Conservative
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SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOLDMAN B S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1175 AA;
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(SLAT/)
(CHEN/)
(GOLD/)
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Matches
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant comprising the recombinant DNA construct and growing the transformed plant with the recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of concent, improved plant growth and development under at least one stress providing improved lignin production of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved lignin production or improved galactomannan conduction. This sequence represents a bacterial polypeptide used in the printed specification but was obtained in electronic forms from repone to encounty conduction or many conduction and production or the properties of the printed specification but was obtained in electronic forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynuclectide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 74.5; DB 8; Length 1124;
Pred. No. 54;
1; Mismatches 37; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 GLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein encoded by Prokaryotic essential gene #29190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     format from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 GQT-SEFVNQVLEKT-AEGNPTGGLVGLRIP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 GYTLDEIKNDITKKTPASFEPTIDYVVTKIP 399
                                                                                                 Claim 1; SEQ ID NO 19968; 122pp; English.
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06-SEP-2001; 2001US-0094893.
25-0CT-2001; 2001US-034923P.
08-FEB-2002; 2002US-00372851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.5%;
28.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1124 AA;
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Zyskind JW; Xu HH;

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the invention fractive to an isobatcum in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated ontological polypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway conclideration, (7) identifying a compound that inhibits proliferation; (8) required for cellular proliferation or the biological pathway or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that compound that inhibits the product is overexpressed or underexpressed; (12) determining the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits in which the strains is present in a culture or collection of an organism. The antisense nucleic acids are useful for strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for required for proliferation in cells other than S. aureus, S. typhimurium, correction of an organism. The antisense modeled produced acids are useful for the target prokaryotic essential genes. Note: The sequence data for this patent and all act of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the paten
                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid comprising any one of
                                                  Ohlsen KL,
Forsyth RA,
                                                  Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 71587; 1766pp; English.
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                                                  Malone C,
Carr GJ,
                                                     Malone
(ELIT-) ELITRA PHARM INC.
                                                  Zamudio C,
Trawick JD,
                                                                                                                                 WPI; 2003-029926/02.
N-PSDB; ACA47533.
                                                     Wang L,
Wall D,
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Sequence 625 AA;

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                           31; Gaps
DB 6; Length 625;
                           31; Indels
                                                                                                                                     190 PNFFQNETSEDNMYLAQRIMFQIDDML-----TKDMLNE; 223
                                                                                                                    44 VNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQ 84
             21.8%; Pred. No. 33; ive 17; Mismatches
 13.3%; Score 73.5;
                                                          8 RLKKKAQYEANKVKLWGLNTEYDNLLF---
                             Conservative
            Best Local Similarity
Matches 22; Conserval
 Query Match
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ADS30054 standard; protein; 1104 AA
                                                 Bacterial polypeptide #19087.
                                      02-DEC-2004 (first entry)
                         ADS30054;
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Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

RESULT 13

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the invention trates to a recombinate the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant comprising an improved property comprises transformed plant with the recombinant DNA construct and growing the transformed plant with the recombinant DNA construct is useful for improving plant with the crompleotide or polypeptide is useful for producing plants with the improved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by addification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and evelopment of carbohydrates one free scope of the invention. Note: The sequence data for this patent did not form, at the printed specification but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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pathogen tolerance, pest tolerance, plant disease resistance, cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to a recombinant DNA construct comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8; Length 1104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 GYTLDEIRNDITKKTPASFEPTIDYVVTKVP 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 19087; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                         21-FEB-2002; 2002US-0360039P.
                                                                                                                                                                                                                                                                20-FEB-2003; 2003US-00369493
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                                                                                                                                                                                                                                                                                                                                                                                                                    CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                      HINKLE G J.
SLATER S C.
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                                                                                                                                                                            US2003233675-A1.
                                                                                                                                                                                                                     18-DEC-2003.
                                                                                                                                   Bacteria.
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                                                                                                                                                                                                                                                                                                                                                    CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                          (GOLD/)
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                                                                                                                                                                                                                                                                                                                                                                           (HINK/)
                                                                                                                                                                                                                                                                                                                                                                                                 (SLAT/)
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GLVGLRIPISKV 108
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                                                                                                                 RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A novel receptor interacting factor (AAW18226) is designated SWRT, i.e. silencing mediator (co-repressor) for retinoic acid receptor (RRK) and thyroid hormone receptor (TR). Its association with RAK and TR both in solution and on DNA response elements is destabilised by ligand. The interaction of SMRT with mutant receptors correlates with the transcriptional silencing activities of receptors. In vivo, SMRT unctions as a potent co-repressor. A GAL4 DNA binding domain fusion of SMRT behaves as a frank repressor of a GAL4-dependent reporter. These data identify a novel class of cofactor which is believed to repersent an important mediator of hormone action. Full-length cDNA for SMRT has been isolated from a HeLa library in a two-hybrid screen using a GAL4 DNA binding domain/RXR fusion protein as bait
                                                                                                                                                                                                        for retinoic acid and thyroid hormone receptor; SMRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1333. .1376
/note= "alternatively spliced insert not present in the original two-hybrid clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New co-suppressor of steroid-thyroid hormone receptor activity - also methods for identifying compounds that relieve its suppressant effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= SG region
061. .1132
label= glutamine-rich region
                                                                                                                                                                                                                                                                                                                                                                                   'note= "proline-rich domain"
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/label= C-terminal_region
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label= N-terminal_region
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                                      AAW18226 standard; protein; 1495 AA
                                                                                                                                                                                                                                                                                                                                                                                                                73. .790
| Tabel = ERDR_region
                                                                                                                                                                                                                                                                                                                          cocation/Qualifiers
                                                                                                                                                                        Transcriptional co-repressor SMRT.
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                                                                                                                                                                                                                   Silencing mediator for retin
transcriptional co-repressor
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Matches 22, Conservative
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                                                                                                                                 (first entry)
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                                                                                      AAW18226
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                         AAW18226
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37 NSIKOBIVNRVONPRDERGPNMGOKLEILIKDTLGLPVAGOTSEFVNOVLEKTAEGNPTG 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood WI;
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pharmaceutical composition for diagnosing or treating psoriasis in a
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Best Local Similarity 30.6%; Pred. No. 1.5e+02;
Matches 22; Conservative 14; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU61812 standard; protein; 2507 AA.
                                                                                                                                                                                                                                             Antipsoriatic protein sequence #347.
                                                                                                                   ADN04305 standard; protein; 2000 AA.
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|GSITKGIPSTRV 1217
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184 GSITKGIPSTRV 195
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N-PSDB; ADN04304.
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Wu TD;
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37 NSIKOBIVNRVONPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTG

96

Homo sapiens.

cancer

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The invention relates to an isolated SWRTe nucleic acid molecule. The nucleic acids are useful in gene therapy, as hybridisation probes for identifying SWRTe-encoding nucleic acid molecules and as primers for amplifying of SWRTe nucleic acid molecules and as primers for simunogens to raise anti-SWRTe antibodies. The polypeptides are useful as immunogens to raise anti-SWRTe antibodies. The SWRTe molecules are useful as targets for discovering and developing modulating agents to predictive medicine, in therapeutic or prophylactic treatment, in chromosome mapping, tissue typing and in forensic identification of a biological sample. Modulators of SWRTe are useful for treating or preventing a condition associated with aberrant SWRTe protein or nucleic acid expression or activity, such as cancer. The present sequence represents the amino acid sequence of the human nuclear receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New SMRTe proteins and nucleic acids, useful in gene therapy, predictive medicine, therapeutic or prophylactic treatment, chromosome mapping, tissue typing and in forensic biology.
                                                                                                                   166. 206
/label= Amphipathic_helix
/note= "Residues 172, 179, 186, 194 and 200 make up the
hydrophobic heptad repeat"
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                                                                                                                                                                                   130. 186
/label= SANT_A_domain
                                                                                                                                                                                                                    613. .669
/label= SANT_B_domain
                                                                 Location/Qualifiers
                                                                                 166. .429
/label= SNC_domain
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                                                                                                                                                                                                                                                                                                                                           27-MAR-2001; 2001US-00819104.
                                                                                                                                                                                                                                                                                                                                                                         29-MAR-2000; 2000US-0193138P
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N-PSDB; ACA62249, ACA62250.
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                                                                                                                                                                                                                                                                         US2003027137-A1
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g ઠે Search completed: February 28, 2006, 08:45:11 Job time : 39.9925 secs

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37 NSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTG 96

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RESULT 1
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Sequence 41799, A
Sequence 57041, A
Sequence 1, Appli
Sequence 3809, Ap
Sequence 2845, Ap
Sequence 2845, Ap
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1368, Ap Ap
24, Ap Ap
26, Appl
2774, A
22834, A
6456, Ap
6456, Ap
8138, Ap
8624, Ap
8624, Ap
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Sequence 3011, Ap
Sequence 16967, A
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960.804 Million cell updates/sec
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1 KLAFRACRLKKKAQYEANKV.....TAEGNPTGGLVGLRIPTSKV 108
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/F_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-914-375C-24
US-08-914-375C-24
US-09-248-796A-14799
US-09-605-703B-2774
US-09-134-000C-553
US-09-13-999C-8138
US-09-513-999C-8138
US-09-270-767-32398
US-09-949-016-8624
US-09-69-949-016-8624
US-09-69-916-8624
US-09-69-916-8624
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US-09-337-384-1
US-005-583-110-3809
US-09-107-433-2845
US-08-914-375C-25
US-09-328-352-5821
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US-09-270-767-41799
US-09-270-767-57041
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                                                                                                                                 US-10-717-665A-44_COPY_532_639
                                                                                                                                                                                                                           572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
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Match Length DB
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11503, A
7458, Ap
2, Appli
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SSETWARE: Patentin Ver. 2.0
SEQ ID NO 41799
LENGTH: 141
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Patent No. 6657054
GENERAL INFORMATION:
APPLICANT: Origine Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE PATENTING DATE: 5002-06-10
SOFTWARE PATENTING DATE: 5002-06-10
SOFTWARE PATENTING DATE: 5002-06-10
SOFTWARE PATENTING DATE: 2002-06-10
SOFTWARE PATENTING DATE: 2002-06-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
US-09-809-665A-18

US-09-809-665A-103

US-09-107-532A-3748

US-09-902-540-11503

US-09-328-352-7458

US-08-742-026-2

US-08-742-026-2

US-08-206-551-54

US-08-206-551-54

US-09-668-482-2

US-09-668-482-2

US-09-668-482-2

US-09-206-551-45

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US-09-206-551-45

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US-09-206-551-45

US-09-248-796A-18593

US-09-248-796A-18593

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Best Local Similarity 100.0%; Pred. No. 2.3e-60;
Matches 108; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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; Sequence 41799, Application US/09270767
; Patent No. 6703491
; GRNERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Drosophila melanogaster
    589
1643
1068
1088
1088
1088
4492
4492
4492
178
178
2106
2106
502
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CRCANISM: Homo sapiens
US-10-164-595-44
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Matches
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                                                       1 KLAFRACRLKKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ 60
                                                                                 35 KLASRACRLKKKRAQHEANKIKLFGLEIEHKRLMNGIAELKQALVVK-----HRTKNLGE 88
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57041
LENGTH: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Evans, Tonald M.
APPLICANT: Evans, J. Don
TITLE OF INVENTION: TRANSCRIPTIONAL CO-REPRESSOR THAT
TITLE OF INVENTION: INTERACTS WITH NUCLEAR HORMONE RECEPTORS AND USES
TITLE OF INVENTION: THERFOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
ADDRESSEE: Pretty, Schroeder, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 KLASRACKLKKKAQHEANKIKLFGLEIEHKRLMNGIAELKQALVVK-----HRTKNLGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KLE-----ILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KLE-----ILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
36.7%; Score 202; DB 2; Length 141;
Best Local Similarity 43.6%; Pred. No. 2.2e-17;
Matches 48; Conservative 17; Mismatches 31; Indels
                 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: 01-SEP-1995
43.6%; Pred. No. 2.2e-17;
tive 17; Mismatches 31
                                                                                                                                                                                                                                                                                             Sequence 57041, Application US/09270767
Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08522726B; Patent No. 6489441; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Drosophila melanogaster US-09-270-767-57041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
                      48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
  Best Local Similarity
Matches 48; Conserv
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TRANSCRIPTIONAL CO-REPRESSOR THAT INTERACTS WITH NUCLEAR HORMONE
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Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
ITILE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
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                                                                                                                                                                                                                                                                                                                                                                                                  37 NSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTG
                                                                                                                                                                                                                                                                                                                                                            37 NSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                      17; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.3%; Score 73.5; DB 2; Length 1495; 30.6%; Pred. No. 9.1; tive 14; Mismatches 17; Indels 19
                                                                                                                                                                                                                                                                              Length 1495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 30.6%; Pred. No. 9.1;
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CURRENT APPLICATION NUMBER: 2000-05-26
CURRENT FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TRANSCRIPTIONAL CO-1
TITLE OF INVENTION: RECEPTORS
FILE REFERENCE: SALK1510-2
CURRENT APPLICATION NUMBER: US/09/337,384
CURRENT FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 08/522,726
REFERENCE/DOCKET NUMBER: P41 90042
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
TELEPAK: 619-546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1495 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1995-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.39
Best Local Similarity 30.69
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 GLVGLRIPTSKV 108
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184 GSITKGIPSTRV 195
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184 GSITKGIPSTRV 195
                                                                                                                                                                                                                                                                                                                           22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 GLVGLRIPTSKV 108
                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn v
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US-09-583-110-3809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
LENGTH: 1495
                                                                                                                                                                                                                                         US-08-522-726B-1
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OTHER INFORMATION: ENPL HUMAN ENDOPLASMIN PRECURSOR (94 KD GLUCOSE- REGULA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 DKIRLISLIDE--NAL---SGNEELTVKIKCDKEKNLLHVTDTGVGMTREELVKN-LGT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 NKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDER-----GPNMGQKLEILIKDTLGL
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                        Indels 31;
                                                                                                                                                                                                  22 LWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM-----GOKLEILI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Steven A. Benner
Applications of Protein Structure Predictions
NUMBER OF SEQUENCES: 74
                                                                                                               Length 651;
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                                                                                                          ; Score 72.5; DB 2;
; Pred. No. 3.7;
12; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.5%; Score 69; DB 2; 27.3%; Pred. No. 2.3; tive 19; Mismatches 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States
ZIP: 32605-4147
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,375C
NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...651
SEQUENCE DESCRIPTION: SEQ ID NO: 2845:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 PVAGOTSEFVNOVLEKTAEGNPTGGLVG 100
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SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                      566 RKDFTIGLPVAGIYEEVWNTELEE 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEES Steven A. Benner
STREET: 1501 NW 68th Terrace
CITY: Gainesville
                                                                                                                                                                                                                                                                                               67 -KD-TLGLPVAGQTSEFVNQVLEK 88
                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-914-375C-25; Sequence 25; Application US/08914375C; Patent No. 6377893; Patent No. 6377893; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-Aug-1997
CLASSIFICATION: 702/20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 352 392 7773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 352 331 0462 INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: amino acid
ORIGINAL SOURCE:
                                                                                                            Query Match 13.2%;
Best Local Similarity 31.0%;
Matches 26; Conservative 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 27.3
Matches 24; Conservative
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                                                                US-09-107-433-2845
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TITLE OF INVENTION: NUCLETC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                          Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                      22 LWGLNTEYDNLLFVINSIKOEIVNRVQNPRDERGPNM------GOKLEILI-
                                                                                                                                                                                                                                                                                                 Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                            Query Match 13.2%; Score 72.5; DB 2; Sest Local Similarity 31.0%; Pred. No. 3.7; Matches 26; Conservative 12; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: <URNOWN>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                    PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR PILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
LENGTH: 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
      US 09/107,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      557 RKDFTIGLPVAGIYEEVWNTELEE 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 -KD-TLGLPVAGQTSEFVNQVLEK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2845, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2845:
                                                                                                                                                                                                                              ORGANISM: Streptococcus pneumoniae US-09-583-110-3809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 651 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
      PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-09-107-433-2845
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APPLICANT: Steven A. Benner
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                                                                          GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO S 5821
LENGTH: 2504
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12.3%; Score 67.5; DB 2; Length 150;
Best Local Similarity 29.4%; Pred. No. 2;
Matches 30; Conservative 11; Mismatches 32; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Mittanck, Cindy A.
APPLICANT: Ww. Yonnie S.
TITLE OF INVENTION: ALL'-fungal Proteins and Methods for Their Use
FILER REPERENCE: 38-21(15036) B.
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT APPLICATION NUMBER: US 60/169,513
PRIOR PILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
12.3%; Score 68; DB 2; Length 2504;
Best Local Similarity 26.6%; Pred. No. 93;
Matches 25; Conservative 10; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---RGPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1731 GEKLNIIGGAAASTPVAKTSGE--NVITRTTODG 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEG 92
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Patent No. 6573361
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; Patent No. 6377893
; GENERAL INFORMATION:
                              Sequence 5821, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OKGANISM: Methanococcus jannaschii
US-09-732-210-1368
                                                                                                                                                                                                                                                                                                                            GRGANISM: Acinetobacter baumannii
US-09-328-352-5821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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US-08-914-375C-24
             US-09-328-352-5821
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OTHER INFORMATION: ENPL_CANFA ENDOPLASMIN PRECURSOR (94 KD GLUCOSE- REGULA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26 Application US/08914375C
Sequence 26 Application US/08914375C
Patent No. 6377893
GENERAL INFORMATION:
APPLICANT: Steven A. Benner
Applications of Protein Structure Predictions
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSE: Steven A. Benner
STREET: 1501 NW 68th Terrace
CITY: Gainesville
Applications of Protein Structure Predictions NUMBER OF SEQUENCES: 74 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLAFRACRLKKKAQYBANKVKLWGLNTEYDNLLFVINSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                 COUNTRY SAGOS-4147

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,375C
FILING DATE: 19-Aug-1997
CLASSIFICATION: 702/20
TELECOMMUNICATION INFORMATION:
TELEFRAX: 352 392 7773
TELEFRAX: 352 331 0462
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.3%; Score 67.5; Di
Best Local Similarity 20.2%; Pred. No. 3.5;
Matches 26; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 32605-4147
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN) (GRP94)
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-914-375C-24
                                                                         ADDRESSEE: Steven A. Benner
STREET: 1501 NW 68th Terrace
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: amino acid
ORIGINAL SOURCE:
ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States
                                                                                                                                                                       COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinston: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANT TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-06-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
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207 ANYYLSKEYIWILYSGVNTYYERFGFKSFPMDFYEVPNTLLTNDVESAIENLIKESKEEK 266
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                                                                                                                          APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Coskar
APPLICANT: Schroder, Caregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
FILE REPERENCE: BG1-126°P
CURRENT FILING DATE: 2000-06-27
CURRENT APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 2774

LENGTH: 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 66.5; DB 2; Length 356;
Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 12.2%; Score 67; DB 2; Length 481; 1 Similarity 22.8%; Pred. No. 12; 21; Conservative 21; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 LIKDT---LGLP-----VAGOTSEFVNQVL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  867 QLPSGKSIRLLLGDN---PADQEIIQFILQ 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.1%; Score 66.5; D
Best Local Similarity 21.1%; Pred. No. 9.1;
Matches 19; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 GPNMGQKLEILIKDTLGLPVAGQTSEFVNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22834, Application US/09248796A Patent No. 6747137
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                                    Sequence 2774, Application US/09605703B Patent No. 6962989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Corynebacterium glutamicum
                                                                                                           APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-248-796A-22834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Ketih Weinstock et al
APPLICANT: Ketih Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
PILE REPERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                  )

OTHER INFORMATION: ENPL MOUSE ENDOPLASMIN PRECURSOR (94 KD GLUCOSE- P11427

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-08-914-375C-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S KFAFQA-----EVNRMMKLIINSLYKNKEIFLRELISNASDALDKIRLISLTDENA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 ---KQEIVNRVQNPRDER-----GPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GPNMGQKLEILIKDTLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.3%; Score 67.5; DB 2; Length 223; 20.2%; Pred. No. 3.5; tive 23; Mismatches 41; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 756;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 LNTE-YD--NLLFVINSI----KOEIVNRVQNPRDER----
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Pred. No. 20;
3; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 LPVAGQTSEFVNQVLEKTAE-GNPTGGLVG 100
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                          APPLICATION NUMBER: US/08/914,375C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14799
LENGTH: 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14799, Application US/09248796A Patent No. 6747137
                                         FILING DATE: 19-Aug-1997
CLASSIFICATION: 702/20
TELECOMMUNICATION INFORMATION:
TELEFAX: 352 392 7773
TELEFAX: 352 331 0462
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: amino acid
CURRENT APPLICATION DATA:
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30.0%;
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Matches 26; Conserva
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Matches 27; Conserv
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US-09-248-796A-14799
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Search completed: February 28, 2006, 08:56:08 Job time : 9.54323 secs

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Sequence 47201, A Sequence 2234, Ap Sequence 22667, A Sequence 19968, A Sequence 1987, A Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 654, Ap Sequence 654, Ap Sequence 104793, Sequence 3555, Sequence 3555, Ap Sequence 3555, Ap Sequence 3555, Ap Sequence 3555, Ap Sequence 3555, Ap
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6933, Ap
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23307, A
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Sequence 31914, A
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Sequence 12, Appl
                                                                                                                                                     February 28, 2006, 08:54:36; Search time 31.4887 Seconds (without alignments) 1433.071 Million cell updates/sec
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(gqn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

(gqn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-450-763-59634
US-10-282-122A-47201
US-10-472-928-2334
US-10-369-493-19968
US-10-369-493-19968
US-10-369-493-19967
US-10-369-493-19087
US-10-369-493-19087
US-10-369-493-19087
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US-10-723-866-1740
US-10-087-192-654
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US-10-087-192-654
US-10-369-493-3509
US-11-369-493-5251
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Listing first 45 summaries
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Sequence 4, Appli
Sequence 4, Appli
Sequence 380, App
Sequence 5897, Ap
Sequence 6103, Ap
Sequence 2706, Ap
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EXPRESSION OF 10,000 OR MORE
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; Sequence 44, Application US/10717665
; Publication Wo. US20050106579A1
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies, Inc.
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; TITLE NEFERENCE: 1U 103 R1
; CURRENT APPLICATION NUMBER: US/10/717,665
; PRIOR APPLICATION NUMBER: US/10/164,595
; PRIOR PLIING DATE: 2002-10-10
; NUMBER OF SEQ ID NO'S: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 639
; TYPE: PRT
; ORGANICEM: Home sapiens
                                                                                                                                                                                                                                                                                                                                                       Sequence 514
Sequence 79,
Sequence 78,
Sequence 2,
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US-10-415-868-2
US-10-282-122A-74571
US-09-968-436B-4
US-10-260-104B-4
US-10-781-014-380
US-09-781-014-380
US-09-781-014-380
US-10-369-493-8103
US-10-369-493-8103
US-10-264-049-2706
US-09-759-010-7
US-10-264-36B-2
US-10-233-553-3
US-10-260-104B-2
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US-11-097-143-31914
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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      Publication No. US20040029129A1
                                                                                                                                                             Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Matches 24; Conserva
                          GENERAL INFORMATION
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US-10-472-928-2234
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                                                                                                                                                                                                                                                                                                                                                                                                              36.7%; Score 202; DB 6; Length 814; 43.6%; Pred. No. 6.6e-14;
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Publication No. US20050196754A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

PILER REFERENCE: 790C1P3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR PILING DATE: 2001-03-30

PRIOR PLICATION NUMBER: 09/540,217

PRIOR PLICATION NUMBER: 09/649,167

PRIOR PLICATION NUMBER: 09/649,167

PRIOR PLING DATE: 2000-03-31

PRIOR PLING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CLUSTOM

SEQ ID NO 59634
                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/194,831
PRIOR APPLICATION NUMBER: 60/194,637
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SQOTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 31914
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 43.6*
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Homo sapiens
US-10-450-763-59634
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Matches 46; Conserr
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: DROSOPHILA
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US-10-450-763-59634
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US-10-282-122A-47201 : j Sequence 47201, Application US/10282122A

RESULT 4

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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REPRENCE: 38-10(52062)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLICING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 GLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 1124;
                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)..(1124); OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-19968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 GYTLDEIKNDITKKTPASFEPTIDYVVTKIP 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.5%; Score 74.5; Di
Best Local Similarity 28.6%; Pred. No. 48;
Matches 26; Conservative 11; Mismatches
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-06
PRIOR PELING DATE: 2000-05-09
PRIOR PILING DATE: 2000-05-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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PRIOR PILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: No. US20030233675Altoc punctiforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 71587, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
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Zyskind, Judith
Wall, Daniel
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Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
Chen, Xianfeng
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Carr, Grant
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NAME/KEY: unsure
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22667
LENGTH: 1175
                                                                                                                                                                                                                                                                                                                                                                                                            2 LAFRACRLKKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 VCLNSCRFYNETRSQLREKRFFVGXNLYINILFLISNVKRIRASRNQDNRPERQSRL-QR 96
                                                                                                                                                                                                                                                                                                                                                                              9 LKKKAQYEANKVK-----LWGLNTEYDNLLFVINSIKOEIVNRVQNPRDERGPNM--
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                                                                                                                                                                                                                                                                         DB 5; Length 345;
                                                                                                                                                                          ; OTHER INFORMATION: 1,4-alpha-glucan branching enzyme-related
US-10-472-928-2234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 ----GOKLEILI-----KD-TLGLPVAGQTSEFVNQVLEK 88
                                                                                                                                                                                                                                                                                                                           20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: (1)..(1175)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                      Query Match
13.7%; Score 75.5; Di
Best Local Similarity 27.6%; Pred. No. 7.6;
Matches 29; Conservative 17; Mismatches
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; Sequence 19968, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22667, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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                                                                                                             TYPE: PRT ORGANISM: Streptococcus pneumoniae
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Best Local Similarity
Matches 23; Conserv
  NUMBER OF SEQ ID N
SOFTWARE: SEGWin99
SEQ ID NO 2234
LENGTH: 345
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                                                                                                                                                                    FEATURE:
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Gaps

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APPLICANT: Hur, Eugene
APPLICANT: Buber, Ben
TITLE OF INVENTION: Inhibitors for Androgen Antagonist Refractory Prostate Cancer
TITLE OF INVENTION: Inhibitors for Androgen Antagonist Refractory Prostate Cancer
FILE REFERENCE: 061040-0018-US
CURRENT APPLICATION NUMBER: US 103/10/705,165
CURRENT APPLICATION NUMBER: US 60/29,956
PRIOR APPLICATION NUMBER: US 60/079,956
PRIOR APPLICATION NUMBER: US 60/113,146
PRIOR APPLICATION NUMBER: US 60/113,146
PRIOR PILING DATE: 1998-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-13-30
PRIOR PILING DATE: 1999-13-30
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Best Local Similarity 30.6%; Pred. No. 91;
Matches 22; Conservative 14; Mismatches 17; Indels 19;
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             CURRENT APPLICATION NUMBER: US/10/351,750
CURRENT FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: US/09/337,384
PRIOR FILING DATE: 1999-06-21
PRIOR PLING DATE: 1995-09-01
PRIOR PLING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/10705165
Publication No. US20050202440A1
GENERAL INFORMATION:
APPLICANT: Fletterick, Robert
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184 GSITKGIPSTRV 195
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REFERENCE: SALK1510-2
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ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                    LENGTH: 1495
TYPE: PRT
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US-10-705-165-26
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Publication No. US20030138836A1
GENERAL INFORMATION:
APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES
APPLICANT: EVANS, RONALD
APPLICANT: EVANS, RONALD
TITLE OF INVENTION: RECEPTORS
TITLE OF INVENTION: RECEPTORS
TITLE OF INVENTION: RECEPTORS
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goodman, Barry S.
APPLICANT: Chen, Xianfeen
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10(52.052)8
FILE REPERENCE: 38-10(52.052)8
CURRENT PALLION NUMBER: US/10/369,493
CURRENT PLING DATE: 2003-02-28
PRIOR PLLING DATE: 2003-02-28
PRIOR PLLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19087
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                                                                                                                                                                                                                                                                                                                                                                                    31; Gaps
  Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 71587
LENGTH: 625
TYPE: PRI
ORGANISM: Staphylococcus haemolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
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                                                                                                                                                                                                                                                                                                                                Query Match 13.3%; Score 73.5; DB 4; Length 625; Best Local Similarity 21.8%; Pred. No. 28; Matches 22; Conservative 17; Mismatches 31; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 PNFFONETSEDNMYLAORIMFOIDDML-----TKDMLNE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 VNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 GQT-SEFVNQVLEKT-AEGNPTGGLVGLRIP 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.3%; Score 73.5; D 27.5%; Pred. No. 61; tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             8 RLKKKAQYEANKVKLWGLNTEYDNLLF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-369-493-19087

; Sequence 19087, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:
                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE
DOCATION: (608)...(608)
CTHER INFORMATION: X=any amino acid
US-10-282-122A-71587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 27.5<sup>3</sup>
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Anabaena PCC7120
US-10-369-493-19087
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Publication No. US20020182586A1
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Matches 22; Conserva
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Glotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions of TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR PPLING DATE: 2002-11-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.3%; Score 73.5; DB 3; Length 2507; Best Local Similarity 30.6%; Pred. No. 1.8e+02; Matches 22; Conservative 14; Mismatches 17; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Indels 19; Gaps
                               Sequence 2, Application US/09819104A

Publication No. US20030027137A1

GENERAL INFORMATION:
APPLICANT: Chen, J. Don
TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: UMG-030

CURRENT APPLICATION NUMBER: US/09/819,104A

CURRENT FILING DATE: 2001-03-27

PRIOR FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.0
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30.6%; Pred. No. 1.8e+02;
tive 14; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-723-860-1740
; Sequence 1740, Application US/10723860
; Publication No. US20040253606Al
; GENERAL INFORMATION:
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US-10-087-192-654
; Sequence 654, Application US/10087192
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SOFTWARE: Patentin version 3.2
SEQ ID NO 1740
LENGTH: 2507
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Best Local Similarity 30.6%
Matches 22; Conservative
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1196 GSITKGIPSTRV 1207
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1196 GSITKGIPSTRV 1207
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ORGANISM: Homo sapiens
US-10-723-860-1740
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    2507
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                        -09-819-104A-2
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US-10-20-2845
US-10-617-320-2845
Sequence 2845, Application US/10617320
Sequence 2845, Application US/10617320
Publication No. US20050136404A1
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: THERAPEUTICS
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.3%; Score 73.5; DB 4; Length 2517; 30.6%; Pred. No. 1.8e+02;
GENERAL INVOCATAILOR:

APPLICANT: MORIEL CAPE

APPLICANT: Engelhard, Eric K.

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: CANCER

FILE REFERENCE: 52945200112

CURRENT APPLICATION NUMBER: US/10/087,192

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 2059

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: FastSEQ for Windows Version 4.0

TYPE: PRT

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/617,320
FILING DATE: 10-Jul-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085131
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
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REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
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TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Waltham
STATE: Massachusetts
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 31.0%; Pred. No. 39;
Matches 26; Conservative 12; Mismatches 15; Indels 31; Gaps
INFORMATION FOR SEQ ID NO: 2845:

SEQUENCE CHARACTERISTICS:

LENGTH: 651 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

ONCECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

LOCATION: (B) LŌCATION 1...651

SEQUENCE DESCRIPTION: SEQ ID NO: 2845:

US-10-617-320-2845
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566 RKDFTIGLPVAGIYEEVWNTELEE 589
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Search completed: February 28, 2006, 09:02:04 Job time : 32.4887 secs

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Sequence 2, Application US/10962951
Publication No. US20060029610A1
GENERAL INFORMATION:
APPLICANT Gidalevicz, Tali
APPLICANT: Biswas, Chhanda
APPLICANT: Simen, Brigitte B.
APPLICANT: Wanderling, Sherry
APPLICANT: Ostrovsky, Olga
TITLE OF INVENTION: GRP94-BASED COMPOSITIONS AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-962-951-2
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Sequence 142, App
Sequence 1269, Ap
                                                                                                                                                                           (without alignments)
556.876 Million cell updates/sec
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                                                                                                                                                    February 28, 2006, 08:56:26; Search time 2.88722 Seconds
                                                                                                                                                                                                                                                                                                          1 KLAFRACRLKKKAQYEANKV......TAEGNPTGGLVGLRIPTSKV 108
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1: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

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7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-962-951-2

US-10-812-234-901

US-10-87-557-314

US-10-467-657-314

US-11-087-719-15

US-11-087-719-14

US-11-087-719-13

US-11-087-719-13

US-11-087-719-14

US-11-072-175-143

US-11-055-822-308

US-11-055-822-308

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US-11-052-951-15

US-10-962-951-17
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551
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    protein search, using sw model
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Maximum DB seq length: 2000000000
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64.5
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Sequence 1643, Application US/10821234

Sequence 1643, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labate, Ivan

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-07

FRIOR APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PL SEQ Genes Version 1.0

SEQ ID NO 1643

LENTH: 803
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180, App
19, Appl
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                 US-10-878-556A-85
US-11-121-130
US-10-48-51-170
US-11-024-959-393
US-11-064-959-393
US-11-108-746-5
US-11-198-746-5
US-11-122-443-180
US-11-122-443-199
US-11-122-443-179
US-11-120-308-80
US-11-120-308-80
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US-11-138-746-8
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Best Local Similarity 27.33
Matches 24; Conservative
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ORGANISM:
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Sequence 3272, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
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ORGANISM: Neisseria gonorrhoeae
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US-10-467-657-314
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TITLE OF INVENTION: HCV regulated protein expression
FILE REFERENCE: 2176-
CURRENT APPLICATION NUMBER: US/10/878,556A
CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
SOFTWARE: Patentin version 3.1
SEQ ID NO 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:

COTHER INFORMATION: amino acid sequence human GRP94
US-10-962-951-2
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw hum/rrb1_human
DATABASE ENTRY DATE: 2003-02-28
                   FILE REPERENCE: 3460-CHOP.C-206US
CURRENT APPLICATION NUMBER: US/10/962,951
CURRENT FILING DATE: 2004-10-12
PRIOR APPLICATION NUMBER: US/10/844,711
PRIOR FILING DATE: 2004-05-12
PRIOR PILING DATE: 2003-05-12
PRIOR FILING DATE: 2003-06-12
PRIOR FILING DATE: 2003-06-12
PRIOR FILING DATE: 2003-06-12
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; Sequence 136, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
USE THEREOF
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   TITLE OF INVENTION:
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Sequence 901, Application US/10821234 Publication No. US20050255114A1

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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Abdarmani, Susan
APPLICANT: Andarmani, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: 0204-04-07
PRIOR PELING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: DL SEQ genes Version 1.0
SEQ ID NO 901
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; Publication No. US2000260581A1
; Publication No. US200050260581A1
; GENERAL INFORMATION:
; APPLICANT: FOURTAM Maria Rita
; APPLICANT: FOURTAM Maria Rita
; APPLICANT: FOURTAM Maria Rita
; APPLICANT: FOURTAM Maria Rita
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR PLLING DATE: 2000-02-12
; NUMBER OF SEQ ID NOS: 9218
; SEQ ID NOS: 9218
; SEQ ID NOS: 9218
; SEQ ID NOS: 9218
; SEQ ID NOS: 9218
; SEQ ID NOS: 9218
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; SEQ ID NOS: 9218
; SEQ ID NOS: 9218
; SEQ ID NOS: 9218
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12.0%; Score 66; DB 6; Length 207;
Best Local Similarity 22.8%; Pred. No. 2.6;
Matches 26; Conservative 17; Mismatches 45; Indels
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APPLICANT: PONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
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APPLICANT: Ochiette, Benoit
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: Alakhov, Valery
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR TREATING DISEASES THAT
TITLE OF INVENTION: INVOLVE ANGIOGENESIS
FILE REFERENCE: PO8605U501/BAS
CURRENT APPLICATION NUMBER: US/11/087,719
FRIOR APPLICATION NUMBER: US 60/555,668
PRIOR FILING DATE: 2004.03-24
                  APPLICANT: Alakhov, Valery
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR TREATING DISEASES THAT
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR TREATING DISEASES THAT
FILLE REFERENCE: PO8605US01/BAS
CURRENT APPLICATION NUMBER: US/11/087,719
CURRENT FILLING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: US 60/555,668
PRIOR FILLING DATE: 2004-03-24
NUMBER OF SEQ ID NOS: 88
SOFTWARE: Patentin version 3.3
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Andamani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
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Pred. No. 5.
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Pred. No. 5.
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CURRENT APPLICATION NUMBER: US/10/821,234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/11087719
Publication No. US20050277575A1
GENERAL INFORMATION:
APPLICANT: Semov, Alexander
APPLICANT: Onichtchenko, Anatoli
APPLICANT: Iourtchenko, Ludmila
Grzegorz
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 43.2%;
Matches 19; Conservative 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 88
SOFTWARE: Patentin version 3.3
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 43.2%;
Matches 19; Conservative 1.
APPLICANT: Pietrzynski,
                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-11-087-719-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-087-719-13
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US-10-821-234-1507
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                                                                                                                                                                                                                                                                                    SEQ ID NO 14
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APPLICANT: Onichtchenko, Anatoli
APPLICANT: Onichtchenko, Ludmila
APPLICANT: Onichtchenko, Ludmila
APPLICANT: Ochiette, Benoit
APPLICANT: Ochiette, Benoit
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: NURENTION: INVOLUB ANGIOGENESIS
FILE PERERENCE: POSGOSUGULBAS
FILE PEPERRENCE: POSGOSUGULBAS
CURRENT APPLICATION NUMBER: US 60/555,668
PRIOR APPLICATION NUMBER: US 60/555,668
PRIOR FILING DATE: 2004-03-24
NUMBER OF SEQ ID NOS: 88
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 GPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 108
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
12.0%; Score 66; DB 6; Length 207;
Best Local Similarity 22.8%; Pred. No. 2.6;
Matches 26; Conservative 17; Mismatches 45; Indels
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                          APPLICANT: MONACI Elisabetta
IIILE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 CRLKNVVWKTLGEVAEYSKNRICSDKLNEHNYVGVDNLL---
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11.9%; Score 65.5; DB 7;
Best Local Similarity 43.2%; Pred. No. 5.2;
Matches 19; Conservative 11; Mismatches 9;
                                                                                             CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 3372
LENGTH: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/11087719
Publication No. US200502775751
GENERAL INFORMATION:
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Sequence 14, Application US/11087719
Publication No. US200502775751
; GENERAL INFORMATION:
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APPLICANT: Onichtchenko, Anatoli
APPLICANT: Iourtchenko, Ludmila
APPLICANT: Ochiette, Benoit
                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3272
  APPLICANT: MASIGNANI Vega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                           FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-087-719-15
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLAFRACRLKKKAQYEANKVKLWG-----LINTEYDNLL-FVINSIKQEIVNRVQNPRD 52
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                                                                                                                           FEATURE:
NAME/KEY: misc feature
LOCATION: (237)...(237)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-207-626A-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pompejus,
APPLICANT: Pompejus,
APPLICANT: Schroder, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REPRENCE: BGI-121CPCN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT APPLICATION DATE: 2056-02-11
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.3%; Pred. No. 6.7;
Matches 21; Conservative 17; Mismatches 34; Indels 1:
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I Similarity 27.5%; Pred. No. 26;
25; Conservative 11; Mismatches
FEATURE:
NAME/KES:
MAME/KES:
MANG/KES:
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PRIOR APPLICATION NUMBER: 09666,740
PRIOR FILING DATE: 2000-06-23
PRIOR PILING DATE: 1999-6-26-5
PRIOR PELICATION NUMBER: 60/141,031
PRIOR PELING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-08-12
PRIOR PILING DATE: 1999-08-12
PRIOR PILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-07-01
PRIOR PELICATION NUMBER: DE 19930476-9
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
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PRIOR FILING DATE: 1999-07-08
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ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 ERGPNMGOKLEILIKDTLGLPVA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 370, Application US/11055822 Publication No. US20050260707A1 GENERAL INFORMATION:
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LENGTH: 1066
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11.9%; Score 65.5; DB 7; Length 339;
Best Local Similarity 43.2%; Pred. No. 5.8;
Matches 19; Conservative 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                           Length 339;
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; Sequence 34, Application US/11207626A
; Publication No. US20060014276A1
GENERAL INFORMATION:
APPLICANT: Havenga, Menzo
; APPLICANT: Hoosels, Ronald
APPLICANT: Bout, Abraham
; TITLE OF INVENTION: CHIMERIC ADENOVIRUSES
; FILE REFERENCE: 2578-4123.2US
; CURRENT APPLICATION NUMBER: US/11/207,626A
; CURRENT APPLICATION NUMBER: EP 98202297.2
; RIOR FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 87
; SQFTWARE: PatentIn version 3.2
; SQF ID NO 34
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.9%; Score 65.5; DE
Best Local Similarity 43.2%; Pred. No. 5.8;
Matches 19; Conservative 11; Mismatches
             CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SEQ ID NO 1507
LENGTH: 339
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US-11-072-175-143
                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-10-821-234-1507
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US-11-072-175-143
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APPLICANT: Schooder, Hartwig
APPLICANT: Schooder, Oskar
APPLICANT: Schooder, Oskar
APPLICANT: Schooder, Oskar
APPLICANT: Baberhauer, Gregor
TITLE OF INVENTION: CONTYBERGENIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REPRENCE: BG1-121CPCN
CURRENT APPLICATION NUMBER: 09/666,740
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR PILING DATE: 1999-00-02
PRIOR PILING DATE: 1999-00-02
PRIOR PILING DATE: 1999-00-02
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APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.9%; Score 65.5; DB 7; Best Local Similarity 27.5%; Pred. No. 26; Matches 25; Conservative 11; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 GYTLDEITNDITGETPAAFEFTIDYVVVKAP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 GQT-SEFVNQVLEKT-AEGNPTGGLVGLRIP 104
76 GOT-SEFVNQVLEKT-AEGNPTGGLVGLRIP 104
                                                           287 GYTLDEITNDITGETPÄAFEPTIDYVVKAP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 1002
                                                                                                                                                                                                                      Sequence 1002, Application US/11055822 Publication No. US20050260707A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Corynebacterium glutamicum
US-11-055-822-1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 368, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
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281 GVDTGGCNIQFAINPVDGRITTIEMNPRVSRSSALASK-----ATGFPIAKMAAKLAI 333
                       FILE OF INVENTION: METABOLIC PATHWAI PROIESINS
FILE OF INVENTION: METABOLIC PATHWAI PROIESINS
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR PILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
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Best Local Similarity 27.5%; Pred. No. 28;
Matches 25; Conservative 11; Mismatches 38; Indels 17;
METABOLIC PATHWAY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 GOT-SEFVNOVLEKT-AEGNPTGGLVGLRIP 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: February 28, 2006, 09:02:41 Job time : 3.88722 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-368
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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y 28, 2006, 08:45:35 ; Search time 6.58647 Seconds	(without alignments) 1577.691 Million cell updates/sec
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February	
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US-10-717-665A-44_COPY_532_639 551 1 KLAFRACRLKKKKAQYEANKV......TABGNPTGGLVGLRIPTSKV 108

Title: Perfect score: Sequence:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de				
Result		Query	:	1	;	
٠ و	Score	Match	Match Length	8	ID	Description
-	82	14.9	571	N	AH2067	two-component hybr
7	83	14.9	902	7	T00072	hypothetical prote
٣	79.5	14.4	534	7	F96713	unknown protein T6
4	78.5	14.2	281	7	E70173	dimethyladenosine
S	76.5	13.9	455	~	865157	hypothetical prote
9	75.5	13.7	642	~	G95129	1,4-alpha-glucan b
7	74	13.4	869	~	A86983	conserved hypothet
8	74	13.4	869	~	S72760	pps1 protein - Myc
Q	73.5	13.3	1104	7	AB2282	carbamoyl phosphat
10	73.5	13.3	1495	~	860255	transcription co-r
11	72.5	13.2	509	7	T08436	inositol-3-phospha
12	72.5	13.2	642	~	E98000	1,4-alpha-glucan b
13	72	13.1	718	~	T49572	related to SHK1 KI
14	71	12.9	505	~	JN0760	H+-transporting tw
15	71	12.9	1355	~	T22552	hypothetical prote
16	70.5	12.8	667	~	S48285	probable glycine-t
17	70	12.7	200	~	AD2116	3
18	70	12.7	846	N	H70871	hypothetical prote
19	69.5	12.6	1105	7	S76557	carbamoyl-phosphat
20	69	12.5	315	~	AH2712	ρ
21	69	12.5	315	~	F97494	
22	69	12.5	330	~	F82338	hypothetical prote
23	69	12.5	803	7	A35954	endoplasmin precur
24	68.5	12.4		7	C34223	<u></u>
25	68.5	12.4		~	E75588	
56	68.5	12.4	552	~	T23171	hypothetical prote
27	68	12.3	258	~	S71561	drought-induced pr
28	68	12.3	1328	~	m	hyrin
29	67.5	12.3	186	7	F64323	ribosomal protein

A;Status: preiminary; translated from GB/EMBL/DDBJ
A;Status: preiminary; translated from GB/EMBL/DDBJ
A;Status: preiminary; translated from GB/EMBL/DDBJ
A;Residues: 1-902 <NAG>
A;Residues: 1-902 <NAG>
A;Cross-references: UNIPROT:060280; UNIPARC:UPI0000178FFB; EMBL:AB011100; PIDN:BAA25454.1
A;Experimental source: brain; clone HG2576
G;Genetics:
A;Note: KIAA0528

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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 12-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 31-Dec-2004
Cispecession: T00072
Establishes (Cispecession)
Cispecession: T00072
Cispecession: T00072
Cispeciation of the coding sequences of unidentified human genes. IX. The complets
A; Reference number: Z14086; MUID:98290545; PMID:9628581
A; Reference number: Z14086; MUID:9629045; PMID:9628581

hypothetical protein KIAA0528 - human

annexin II - rat	probable ubiquinon	endoplasmic reticu	glucose-regulated	protein kinase ppk	heat shock protein	proteoglycan core	aggrecan - bovine	malate oxidoreduct	RNA-directed RNA p	hypothetical prote	hypothetical prote	transcription fact	liver regeneration	annexin II - bovin	transcription regu
833700	F82366	A29317	A53211	S51358	A57513	A39808	T42630	A82232	REXSIB	T34081	T16580	A54025	A39382	LUBO36	B86850
0	~	N	N	~	N	N	~	N	Н	~	~	N	7	н	7
339	544	802	804	804	828	1340	2327	588	878	1130	13055	181	181	339	224
12.3	12.3	12.3	12.3	12.3	12.3	12.3	12.3	12.2	12.2	12.2	12.2	12.1	12.1	12.1	12.0
67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67	67	67	67	66.5	66.5	66.5	99
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

## ALIGNMENTS

AH2067	
two-compone	two-component hybrid sensor and regulator all2094 [imported] - Nostoc sp. (strain PCC 71; C.Species: Nostoc sp. PCC 7120
A; Note: Not C; Date: 14-	A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence revision 14-Dec-2001 #text_change 09-Jul-2004
C; Accession: AH2067	a: AH2067
R;Kaneko, ' Nakazaki,	R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; watanabe, A.; IIIgucui. Nakazaki, N.; Shimpo, S.; Suqimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8,	, 205-213, 2001
A; Title: Co	A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anar a.paforance number: AR1807: MITD:21595285: PMID:11759840
A; Accession: AH2067	n: AH2067
A; Status:	A; Status: preliminary
A;Residues: 1-571 < K	Afroidecule Lype: Juna A:Residues: 1-571 < KUR>
A; Cross-re	A;Cross-references: UNIPROT:Q8YV87; UNIPARC:UPI00000CE2FB; GB:BA000019; PIDN:BAB73793.1; A;Experimental source: strain PCC 7120
C,Genetics: A,Gene: all2094	: 12094
Query Mat	tch 14.9%; Score 82; DB 2; Length 571;
Best Loca Matches	Best Local Similarity 24.2%; Fred. No. 2.4; Matches 24; Conservative 17; Mismatches 38; Indels 20; Gaps 3;
<i>λ</i> ο	23 WGLNTEYD-NLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILLIKD 68
Dp	172 WQFDDAQDRNLTEVVQLIDEQTLNSIQNPIISAIQKETTVYLGDGLSPTVGHRIMLITKD 231
Š	69 TLGLPVAGQTSEFVNOVLEKTAEGNPTGGLVGLRIPTSK 107
 92	

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A;Cross-references: UNIPROT;Q12080; UNIPARC:UP1000013BD31; EMBL:Z73502; NID:g1370311; PII A;Experimental source: strain S288C (AB972) H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; submitted to the EMBL Data Library, December 1995 submitted to the EMBL Data Library, December 1995 A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm. A;Reference number: S69040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Rolecule type: DNA
A, Residues: 1-455 < HAL>
A, Residues: 1-455 < HAL>
A, Residues: 1-455 < HAL>
A, Residues: 1-455 < HAL>
A, Residues: 1-455 < HAL>
A, Coster, F.; Naveau, F.; Goffeau, A.
R, Purnelle, B.; Comblez, S.; Coster, F.; Naveau, F.; Goffeau, A.
Submitted to the RMIL Data Library, March 1996
A, Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifies in the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant A; Reference number: 869428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1,4-alpha-glucan branching enzyme [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPARC:UPI000013BD31; EMBL:X96770; NID:g1403537; PID:g1403563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŝ
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                                                                                                               72
                                                                                                                                                NyAlternate names: hypothetical protein P2610
Cispecies: Saccharomyces cerevisian P2610
Cispecies: Saccharomyces cerevisian 31-May-1996 #text_change 31-Dec-2004
Cispate: 10-Dec-1994 #eequence revision 31-May-1996 #text_change 31-Dec-2004
Cispate: 10-Dec-1994 #eequence revision 31-May-1996 #text_change 31-Dec-2004
Cispate: 10-Dec-1994 #eequence revision 31-May-1996 #text_change 31-Dec-2004
Cispate: 10-Dec-1994 #eequence Database, May 1996
A):Reference number: S65154
A):Accession: S65157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 KKKAQYEANKVK------LWGLNTEYDNLLFVINSIKQEIV-----NRVQNPR
                                                                                                            21 KLWGLNTEYDNLLFVIN-SIKQEIVNRVQNPRDER----GPNMGQKLEILIKDT---LGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Gaps
                                                            Gaps
                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 455;
Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein YPL146c - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Indels
                                                            23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Superfamily: tumor suppressor protein, Gltscr2/p60 type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
      DB 2;
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21; Mismatches
      Query Match
14.2%; Score 78.5; DE
Best Local Similarity 31.6%; Pred. No. 2.3;
Matches 24; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76.5;
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24.8%;
                                                                                                                                                                                                                                                                                 : : || : | : | 84 EIDLKYSEILNEKFGK 99
                                                                                                                                                                                                                                          73 PVAGQTSEFVNQVLEK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Cross-references: SGD:S0006067
A, Map position: 16L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: S69453
A,Molecule type: DNA
A,Residues: 1-455 <PUW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 IPTSK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-455 < PUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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A;Experimental source: strain B31
C;Superfamily: dimethyladenosine transferase (rRNA adenosine dimethyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Spate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C. Spatesion: P65713
R. Species: A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H., Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A, Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Titles: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A, Rocession: F96713
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R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Hanson, M.; Vugt, Sowman, C.; Garland, S.; Fuji, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: More sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: E70173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                    368 RLCRLKKKAQABANA-----TAISNLLPFMEYEVHTQLMNKLK----LKGMNALFGLR 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
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C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 RLKKKKAQY-----EANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQ-----NPRD
                                                                                                                                 5 RACRLKKKAQYEANKVKLWGLNTEYDNLL-FVINSIKQEIVNRVQNPRDERGPN--MGQK
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                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.4%; Score 79.5; DB 2; Length 534; 30.4%; Pred. No. 4;
                     14.9%; Score 82; DB 2; Length 902; 28.4%; Pred. No. 4.3; ive 22; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                          62 LEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                       29; Conservative
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Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Residues: 1-534 <STO>
                                                         Similarity
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A,Map position: 1
                           Query Match
Best Local S:
Matches 29
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C.Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. PCC 7120
A,Note: Nostoc sp. strain PCC 7120
A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C,Accession: AB2282
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A,Fitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840
A,Accession: AB2282
A,Status: preliminary
                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q49689; UNIPARC;UPI000016FA8B; EMBL:U00013; NID:g466868; PID:
A;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: 216918
                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 202-481, A, 483-589 <PAR>
A;Cross-references: UNIPARC:UPI000016FB03; EMBL:Z99125; NID:g2398683; PIDN:CAB16172.1; PJ
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A;Residues: 1-1104 «KUR»
A;Cross-references: UNIPROT:Q8YQL2; UNIPARC:UPI0000126F6F; GB:BA000019; PIDN:BAB75508.1;
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: alr3809
C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carbamoyl phosphate synthetase large chain [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cibate: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
Ciscossion: S60255
Cistocasion: S60255
Richen, J.D.; Evans, R.M.
Nature 377, 454-457, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 RIKKKAQYEANKVKLWGLN---TEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 RLKALRVFERKPMPRWGSNLDGIDFDNIKYFVRSTEKQAASWDELPEDIRN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.4%; Score 74; DB 2; Length 869; 23.6%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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            submitted to the EMBL Data Library, November 1993 A; Description: Mycobacterium leprae cosmid B1496. A; Reference number: S72695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 GQT-SEFVNQVLEKT-AEGNPTGGLVGLRIP 104
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Local Similarity 27.5%; Pred. No. 39;
tes 25; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 23.6%; Pred. No. 26;
Matches 21; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 LIKDTLGLP-----VAGQTSEFVNQVL 86
                                                                                                             A;Accession: S72760
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-869 <SMI>
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Matches
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x;rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A,Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A,Ittle: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A,Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein ML0593 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: As6993
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Axutre 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-642 «KUR»
A;Cross-references: UNIPROT:Q97QS8; UNIPARC:UP10000C9CBF; GB:AE005672; PIDN:AAK75232.1;
A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT:Q49689; UNIPARC:UPI000013AB0A; GB:AL450380; NID:g13092788;
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N,Alternate names: B1496_C2_189 protein
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Bate: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72760; T11013
R;Smith, D.R.; Robison, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 RLKKKAQYEANKVKLWGLN---TEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%; Score 74; DB 2; Length 869; 23.6%; Pred. No. 26; tive 19; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GQKLEILI-----KD-TLGLPVAGQTSEFVNQVLEK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
13.7%; Score 75.5; Di
Best Local Similarity 27.6%; Pred. No. 13;
Matches 29; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SP1121
C;Superfamily: 1,4-alpha-glucan branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - TYDRLGIPDAEKQRLVAGVAAQYESEVV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 LIKDTLGLP-----VAGQTSEFVNQVL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Conservative
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Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-869 <STO>
                                                                                                                                                                                                                                                                                                   A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A86983
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A;Gene: ML0593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SP1121
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NyAlternate names: F1-F0 ATPase beta chain
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text_change 31-Dec-2004
C;Accession: JNO760; S32130; $\overline{5}64699$
R;Pena, P.; Garesse, R.
Biochem. Biophys. Res. Commun. 195, 785-791, 1993
A;Title: The beta subunit of the Drosophila melanogaster ATP synthase: CDNA cloning, amir A;Reference number: JNO760; MuID:93384603; PMID:8373413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UPI000016BAEB; EMBL:X71013; NID:g287944; PIDN:CAA50332.1; PII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T49572
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, Bischulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, A;Reference to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;cross-references: UNIPROT:Q9P5Z7; UNIPARC:UPI000069977; EMBL:AL355930; GSPDB:GN00116; A;Experimental source: BAC clone B208; strain OR74A
                                                                                                                                                                                                                                          C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 RLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRV------QNPRDERGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 6
A;Introns: 45/3; 152/1; 274/1; 658/3
C;Superfamily: Schizosaccharomyces pombe negative regulator of mitosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related to SHK1 KINASE-BINDING protein [imported] - Neurospora crassa
                                                                                   Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.1%; Score 72; DB 2; Length 718; 25.7%; Pred. No. 33; tive 15; Mismatches 30; Indels
                                                                                                                                              Indels
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                                                                                      DB 2;
                                                                                                                                                                                                        22 LWGLNTEYDNLLFVINSIKOEIVNRVQNPRDERGPNM--
C;Superfamily: 1,4-alpha-glucan branching enzyme
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, February 1993
A;Reference number: S32130
A;Accession: S32130
                                                                                   13.2%; Score 72.5; D
31.0%; Pred. No. 26;
tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                || |:|||||| | ||:
557 RKDFTIGLPVAGIYEEVWNTELEE 580
                                                                                                                                                                                                                                                                                                                           67 - KD-TLGLPVAGQTSEFVNQVLEK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N,Alternate names: protein B208.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  +52 IITKLDILVTELLG 465
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Best Local Similarity 25.7%
Matches 19; Conservative
                                                                                                                  Best Local Similarity 31.09
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S8 MGQKLEILIKDTLG
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A; Residues: 6-505 < GAR>
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A; Residues: 1-505 < PEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Gene: NCSP: B208.200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
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C;Genetics:
-A;Gene: g1gB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: catalyzes the reversible isomerization of D-glucose 6-phosphate to 1L-myd C;Superfamily: myo-inositol-1-phosphate synthase C;Keywords: intramolecular lyase; isomerase
                                                                                         A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1495 <CHE>
A;Cross-references: UNIPROT:Q9Y618; UNIPARC:UPI000016A25F; EMBL:U37146; NID:g1045654; Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:Q96348; UNIPARC:UP1000017952A; EMBL:U66307; NID:g1513227; PI
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A,Title: A transcriptional co-repressor that interacts with nuclear hormone receptors. A,Reference number: S60255; MUID:96008552; PMID:7566127
A,Accession: S60255
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CyAccession: B98000
R. Accession: B98000
R. Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.:
R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, Y.
P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-577, 2001
A,Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A,Authors: Yang, Y.; Wung-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A,Title: Genome of the Bacterium Streptococous pneumoniae Strain R6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 EANKVK----LWGLNTE-YDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Brassica napus (rape)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08436
R;Hussain, A.; Bourgeois, J.; Polvi, S.; Tsang, E.; Keller, W.A.; Georges, F. submitted to the EMBL Data Library, August 1996
A;Reference number: Z16418
A;Accession: T08436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Streptococcus pneumoniae
Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                   37 NSIKOEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                          Query Match 13.3%; Score 73.5; DB 2; Length 1495; Best Local Similarity 30.6%; Pred. No. 57; Matches 22; Conservative 14; Mismatches 17; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nositol-3-phosphate synthase (EC 5.5.1.4) [similarity] - rape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 GLPVAGQTSEFVNQVLEKTAEGNPTG----GLVGLRI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-509 <HUS>
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Best Local Similarity 26.8%
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 GLVGLRIPTSKV 108
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GSITKGIPSTRV 195
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A;Molecule type: DNA
A;Residues: 1-642 <KUR>
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Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain

Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthesis; hydrolase; membrane-associated complex; mitochondrion; nud

Stall/Domain: transit peptide (mitochondrion) #status predicted <TNP-

1/32-505/Product: H+-transporting ATP synthase beta chain #status predicted <MAT>

1/183-190/Region: nucleotide-binding motif A (P-loop)

1/209-384/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
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A;Molecule type: DNA
A;Residues: 1-1355 <W12>
A;Cross-references: UNIPARC:UPI000017BCEF; EMBL:Z93398; PIDN:CAB07724.1; GSPDB:GN00019;
A;Experimental source: clone ZK1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Map position: 1
A,Introns: 94/3; 124/3; 150/3; 209/3; 248/3; 311/3; 424/3; 734/2; 934/2; 1104/3; 1167/3
        R;Pena, P.; Ugalde, C.; Calleja, M.; Garesse, R.
Biochem. J. 312, 887-897, 1995
A;Title: Analysis of the mitochondrial ATP synthase beta-subunit gene in Drosophilidae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1355 <WIL>
A;Cross-references: UNIPARC:UPI000017BCEF; EMBL:292788; PIDN:CAB07214.1; GSPDB:GN00019;
                                                                                                                                                                                                                                                     Cross-references: UNIPARC:UPI00012643F; EMBL:X86015
Comment: This enzyme catalyzes the synthesis of ATP coupled to H+ gradient generated
Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.pate: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 29-Oct-1999 C.Accession: T22552; T27703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 IVNRVQNPRDERGP------NMGQKLEILIKDTLGLPV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.9%; Score 71; DB 2; Length 1355;
llarity 24.4%; Pred. No. 90;
Conservative 21; Mismatches 37; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
12.9%; Score 71; DB 2; Length 505;
Best Local Similarity 24.8%; Pred. No. 27;
Matches 31; Conservative 11; Mismatches 21; Indels
                                                                                                                      A;Reference number: S64699; MUID:96128076; PMID:8554535
A;Accession: S64699
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nypothetical protein ZK1151.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, March 1997 A;Reference number: Z19580 A;Accession: T22552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Harris, B.
submitted to the EMBL Data Library, March 1997
Keference number: 220408
A;Accession: T27703
                                                                                                                                                                                                                                                                                                                                                             A,Gene: FlyBase:ATPsyn-beta
A,Cross-references: FlyBase:FBgn0010217
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A; Residues: 1-505 <PE2>
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086dg5 mus musculu

086dg5 mus musculu

041rx3 tetraodon n

07dg21 anopheles g

05dgy2 schistosoma

09vc61 drosophila

080va1 mus musculu

060052 mus musculu

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07tps5 mus musculu

05rdc8 pongo pygma

07nmf2 gloeobacter

05rdc8 pongo pygma

07nmf2 gloeobacter

086v87 anabaena sp

075c19 homo sapien

060280 homo sapien

060280 homo sapien

060280 homo sapien

06136 borreala bu

07xx0 xenopus lae

09cab0 arabidopsis

073x9 bacillus ce

064xt2 bacteroides

09cab arabidopsis

073x9 bacillus ce

064xt2 bacteroides

09cab arabidopsis

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QSCOU3_MOUSE
Q5RDC8_PONPY
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Q738A9 BACCI
Q64XT2 BACFR
Q8966 IBDV
Q9RRR3 FUSNU
YP46 YEAST
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                              1 KLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6J; TISSUE=Testis; MEDLINE=99279273; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                           Gaps
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QBCDGS;

10-MAR-2003 (TrEMBLrel. 23, Last sequence update)

10-MAR-2004 (TrEMBLrel. 25, Last annotation update)

MUS museulus adult male testis cDNA, RIXEN full-length enriched library, clone:4932441F15 product:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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                             61 KLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 108
                                                                                                                                                                                                                                                                                                     Length 639;
                                                                                                                                                                                                                                                                                                     Query Match 97.3%; Score 536; DB 2; Length 63
Best Local Similarity 98.1%; Pred. No. 3.7e-43;
Matches 106; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
Li F., Yao K.T.,
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                  EMBL; AY139008; AAN38956.1; -; mRNA.
InterPro; IPR004827; TF bZIP.
PROSITE; PS00036; BZIP BASIC; UNKNOWN 1.
SEQUENCE 639 AA; 72090 MW; 3A19E0926B9A6406 CRC64;
                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                    639 AA
                                                                                                                       Created)
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                                                                                                                      OBIZG1_HUMAN PRELIMINARY;
                                                                                                                                                    Adult retina protein.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
Name=A930001N09Rik;
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C STRAIN-C57BL/6J; TISSUB=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Rukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Alayshida K., Hayatsu N., Hiramoto K., Hiracka T., Hirozane T., A Hayshida K., Hayatsu N., Hiramoto K., Hiracka T., Hirozane T., RA HOTI F., Imotani K., Ishii Y., Tich M., Kagawa I., Kausukawa T., RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., A Karihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., A Kirihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., A Saito R., Saitoh H., Sakai K., Sakazume N., Sano H., Ragawa A., Takaku-Akahira S., Takada Y., Tagami M., Tomaru A., Toya T., Yasunishi M., Muramatsu M., Hayashizaki Y., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Barak J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., W. Winniaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., B., Warning L., Wanniaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., B., Wanniaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 640;
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40 AA; 72598 MW; FE02C532FA34E1DE CRC64;
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Pred. No. 9.8e-41;
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MGI; MGI:1924378; A930001N09Rik.
InterPro; IPR004827; TF bZIP.
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93.5%;
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ENSANGP0000015170 (Fragment)
ORFNames=ENSANGG0000012681;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae;
                               1 KLAFRACRLKKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=GSTENG00029962001;

Tetraodon nigroviridis (Green puffer).

Tetraodon nigroviridis (Green puffer).

Tetraodon nigroviridis (Green puffer).

Actinopterygii, Neopterygii, Teleostei, Euteleostei; Neoteleostei;

Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                          The German CDNA Consortium;

Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; BX647573; CAI46104.1; -; mRNA.

InterPro; IPR004827; TF bZIP.

PROSITE; PS00036; BZIP BASIC; UNKNOWN_1.
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                                                                                                             KLEILIKDTLGLPVAGQTSEFVNQVLGKTAEGNPTGGLVGLRIPASKV 640
                                                                                             61 KLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 604;
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4; Indels
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 7 SCAF15001, whole genome shotgun sequence.
                                                                                                                                                                                                                                     10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein DKFZp313F2319 (Fragment).
Name=DKFZp313F2319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 64.1%; Score 353; DB 2; Local Similarity 97.2%; Pred. No. 1.8e-25; nes 69; Conservative 1; Mismatches 1;
3; Mismatches
                                                                                                                                                                                                        QSHYKO_HUMAN PRELIMINARY;
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   Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 KLEILIKDTLG
                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
TISSUE=Adipose;
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SEQUENCE
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1 KLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ 60
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skali Z., Cattolico L., Poulain J., De Berardinis V., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kalis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander B.S., Weissenbach J., Roest Crollius H., "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KLEILIKDTLG------LPVAGQT
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
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Submitted (ARF-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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PRT; 293 AA. 07021 AB. 07021 AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB. 07021 OF AB.
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GO: GO:0003677; F:DNA binding; IEA.
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                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 KLASKICKLKKKAFHEANKIKYLGLEIEYNELASVIVRIKELITKYL---RDHLPP 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGP 56
                                                                                                                                                                                                                                                                                                                                                      Han Z.;
"The full-length cDNA sequences of Schistosoma japonicum genes.";
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AX915642; AAW7374.1; -; mRNA.
Hypothetical protein.
SEQUENCE 584 AA; 65536 MW; 385055EP335323CC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.6%; Score 113.5; DB 2; Length 584; Best Local Similarity 50.0%; Pred. No. 0.028; Matches 28; Conservative 6; Mismatches 19; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                              21.8%; Score 120; DB 2; Length 293; 79.3%; Pred. No. 0.003;
                                                                                        Indels
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
10-WAY-2005 (TrEMBLrel. 30, Last annotation update)
CG13624-PA, isoform A (Cg13624-pb, isoform b) (SD09792p)
                                     31535 MW; 0700521A3C593F97 CRC64;
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10-MXY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hyporhetical protein.
Schistosoma japonicum (Blood fluke).
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                                                                                                                                                                                                       584 AA
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                                                                                    4; Mismatches
                                                                                                                              247 KLASRACRLKKKAQHEANKIKLYGLETEH 275
                                                                                                               1 KLAFRACRLKKKAQYEANKVKLWGLNTEY 29
 PS00036; BZIP_BASIC; UNKNOWN_1.
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                    QSD9Y2_SCHJA PRELIMINARY;
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Q9VC61; Q8T9A9;
                                                                          Best Local Similarity 79.38
Matches 23; Conservative
                          293
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NUCLEOTIDE SEQUENCE.
                        293 2
293 AA;
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PROSITE; ENON TER NON TER SEQUENCE
                                                               Query Match
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Ade Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

Fosler C., Gabrielian A.E., Garg N.S., Galbart W.M., Glasser K.,

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Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalai M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,

Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattei B. McIntosh T.C., McLood M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Raine B.C., Siden-Krämos I., Simpson M., Skutpski M.P., Smith T.,

She B.C., Siden-Krämos I., Simpson M., Strong R., Sun E.,

Syrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho Q., Zheng L.,

RA Spier B., Spradling A.C., Stapleton M., Zhong G., Zhao Q., Zheng X.M., Myelson S.M., Woolage T., Worley K.C., Wu D., Yang S., Zhong L.,

RA Shins S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho Q., Zheng X.M., Whye Standers G.M., Venter E.W., Zhong K.J., What Shong W., Zhou X., Zhu S., Zhong X.M., Weinstone Sequence of Drosophila melanogaster.",

Science 287:2185-2195(2000).
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MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., George R.A., Peiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., Finishing a Whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaminker J.S., Bergman C.M., Kroimiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective."; Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
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Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdalle R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase;
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
[7]
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDLINE=22426070; PubMed=12537573;
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5 RACRLKKKRAQYEANKVKLWGLNTEYDNLL-FVINSIKQEIVNRVQNPRDERGPN--MGQK
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                EMBL; BC049905; AAH49905.1; -; mRNA.
Ensembl; ENSWUSGO0000030279; Mus musculus
MGI; MGI:1921991; 5730419109Rik.
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Q8CIDS_MOU
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
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Strausberg R.;
                      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                20.5%; Score 113; DB 2; Length 755; 75.9%; Pred. No. 0.041;
                                                                                                                                                                  Q9VL14:CG18619; NbExp=1; IntAct=EBI-150517, EBI-165049;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                  EMBLY, ASYCGI. -.
IntAct, Q9VGGI. -.
Ensembl; CG13624; Drosophila melanogaster.
ElyBase es F8gn0032909; CG13624.
InterPro; IFR004827; TF bZIP.
PROSITE; PS00036; BZIP BASIC; UNKNOWN I.
PROSITE: ASYCGI MW; D851D42235FF10E5 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   708 KLASRACRLKKKAQHEANKIKLFGLEIEH 736
                                                                                                                                                                                     EMBL, AE003748; AAF56314.2; -; Genomic_DNA
EMBL; AY069850; AAL39995.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Name=5730419109Rik;
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QBOVA1;
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Best Local Similarity 75.9
Matches 22; Conservative
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          NUCLEOTIDE SEQUENCE
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                                                                                                                                              -1- INTERACTION
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CSTRAINE-EVBN N; TISSUB-Ammary tumor. C3;

KEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KITATINE-EVBN N; TISSUB-Ammary tumor. C3;

KITATINE-EVBN N; TISSUB-Ammary tumor. C3;

KITATINE-EVBN N; TISSUB-AMMARIAN E.A., Grouse L.H., Derged J.G.,

RAISCHUI S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hashe F.,

Districhench U., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

An Expleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RANA S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield W. Schein J.E., Jones S.J.M., Marra M.A., Schein J.E.,

But Ammara M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E.,

Butterfield W. Schein J.E., Jones S.J.M., Marra M.A., Schein J.E.,

Butterfield W. Schein J.E., Jones S.J.M., Marra M.A., Schein J.E.,

Butterfield W. Schein J.E., Jones S.J.M., Marra M.A., Schein J.E.,

Butterfield W. Schein J.E., Jones S.J.M., Marra M.A., Schein J.E.,

Butterfield W. Schein J.E., Jones S.J.M., Marra M.A., Schein J.E.,

Butterfield W. Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones W. S.M., Marra M.A., Schein J.E., Jones W. J.M., Marra M.A., Schein J.E., Jones W. J.M., Marra M.A., Schein J.E., Marra M.A., Schein J.E., J. Jones W. J.M., Walley M. J
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                                                                                                                                                                                                                                                                             5 RACRLKKKAQYEANKVKLWGLNTEYDNLL-FVINSIKQEIVNRVQNPRDERGPN--MGQK
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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15.8%; Score 87; DB 2; Length 818;
Best Local Similarity 29.4%; Pred. No. 15;
Matches 30; Conservative 22; Mismatches 26; Indels
                                                                        15.8%; Score 87; DB 2; Length 487; 29.4%; Pred. No. 8.3; tive 22; Mismatches 26; Indels
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Director MGC Project;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 LEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
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SEQUENCE 487 AA; 53277 MW; 9CE3489ADD52AAC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 IQITVGETMLMGLASATGVYLAAL-----PTPG--GIQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Ensembl; ENSMUSG00000330279; Mus musculus.
MGI; MGI:1921991; 5730419109Rik.
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QBCID5;
01-MAR-2003 (TrEMBLrel. 23, La
01-MAR-2004 (TrEMBLrel. 23, La
01-MAR-2004 (TrEMBLrel. 26, La
RIXEN CDNA 5730419109.
Name=5730419109R1k;
                                                                                                                                                                                           30; Conservative
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The state of the

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Name=5730419109Rik;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
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         OGN SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SE
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Nagase T., Ohara O., Koga H.;

"Prediction of the coding sequences of mouse homologues of KIAA gene:
"Prediction of the coding sequences of 500 mouse KIAA-homologous
orn's incomplete nucleotide sequences of 500 mouse KIAA-homologous
orn's incomplete nucleotide sequences of 500 mouse KIAA-homologous
orn's connainal sequences of cDNA clones
orn's connainal sequences of cDNA clones
orn's connainal 1 c2 domain.

I. SIMILARITY: Concainal 1 c2 domain.

Embl., AKI7266; BAD32244.1; -; RRNA.

BEBL; AKI7266; BAD32244.1; -; RRNA.

Remb., AKI7266; BAD32244.1; -; RRNA.

Remb., AKI7266; BAD32244.1; -; RRNA.

Remb., AKI7266; BAD32244.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; BAD3224.1; -; RRNA.

Remb., AKI7266; RRMA.

Remb., AKI7266; RRMA.

Remb., AKI7266; RRMA.

Remb., AKI7266; RRMA.

Remb., AKI7266; RRMA.

Remb., AKI7266; RRMA.

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Remb., AKI7266; RRMA.

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Remb., AKI7266; RRMA.

Remb., AKI7266; RRMA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Gaps
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                                                                                                                                      368 IQITVGETMLMGLASATGVYLAAL-----PTPG--GIQI 399
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                                                                                               62 LEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
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                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
MRAA0528 protein (Fragment).
Name=573041910981k; Synonyms=mKIAA0528;
Mus musculus (Mouse).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                  993 AA
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PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM00239; C2; 1.
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Matches 30; Conservative
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QGA052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7TPSS MOUSE PRELIMINARY;
Q7TPSS;
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PubMed=15368895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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Q7TPS5 MOUSE
1D Q7TPS5 MC
AC Q7TPS5 MC
DT 01-OCT-20
DT 01-OCT-20
DT 01-OCT-20
DT 01-MAR-20
DE 573041910
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CSTRAIN=CSTBL/65; TISSUE=EGG;

KN STRAIN=CSTBL/65; TISSUE=EGG;

KN STRAIN=CSTBL/65; TISSUE=EGG;

KN STRAIN=CSTBL/65; PubMed=12477932; DOI=10.1073/pnas.242603899;

KN STAUBSETG R.L., Feingold B.A., Grouse L.H., Derge J.G.,

KN Clausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerew K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

A patiethench D., Marusina K.B., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Kilalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

Radan A., Felton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U.N.,

Rodeneration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.8%; Score 87; DB 2; Length 1016; 29.4%; Pred, No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUE=Egg;
Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 LEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1016 AA
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QBC0U3;
01-MAR-2003 (TYEMBLYEL: 23,
01-MAR-2004 (TYEMBLYEL: 26,
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RA Arawawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Konoo H., Adachi J., Fukuda S., Alazawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Reischmann M., Gaasterland T., Gissi C., King B., Kochiwa H., Ashell P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suurki R., Tomita M., Wagner L., Washio T., Baka K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whinkaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Marsel, S., V.
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STRAIN=C57BL/6J; TISSUR=Testis;

STRAIN=C57BL/6J; TISSUR=Testis;

A Shibate K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., A Shibate K., Itch M., Aizawa K., Kitsunai T., Tashiro H., Itch M., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., A Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., A Pujiwake S., Inoue K., Togawa K., Tanaka T., Nakaniwagi K., A Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; A Yoneda Y. Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUB=Testis; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.; Nuramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930598116 product:hypothetical C2 domain/C2-domain profile/Synaptoctagmin/Cytochrome c family heme-binding site containing protein, full insert sequence.
Name=5730419109Rik;
                                                                                                                                                                                                                                                                                                STRAIN=CSTBL/6J; TISSUE=Testis; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Rayashizaki Y.; Hayashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001).
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                                                                                                                                       (Mouse)
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                       Mus musculus
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Putuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Ayashida K., Eurino M., Hiraoka T., Hiraoka T., Hiraoka T., Hayashida K., Hayateu M., Hiraoka T., Hiraoka T., Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Koda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nakamura M., Nakamura M., Saltoh H., Sakai T., Shinagawa A., Shiraki T., Soqabe Y., Tagami M., Sasaki D., Saltoh H., Sakai C., Sakizoh H., Sakai C., Shinagawa A., Shiraki T., Soqabe Y., Tanaka T., Yasani B., Yanaya A., Takaku-Akahira S., Takeda Y., Tanaka T., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Yasanishi A., Muramatsu M., Hayashizaki Y.; Tubinited (JUL-2001) to the EMBL/GenBank/DDBJ databases.

SIMILARITY: Contains I CZ domain.

SIMILARITY: Contains I CZ domain.

SIMILARITY: Contains I CZ domain.

BEREL, AKOS925; BARB.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

RO; GO:0006215; F:transporter activity; IEA.

GO; GO:0016215; F:transporter activity; IEA.

RO; GO:0006810; P:transport; IEA.

RO; GO:0006810; P:transport; IEA.

RO; GO:0006810; P:transport; IEA.

RO; GO:0006810; P:transport; IEA.

RO; GO:0006810; P:transport; IEA.

RO; GO:0006810; P:transport; IEA.

RO; GO:0006810; P:transport; IEA.

RO; GO:0006810; P:transport; IEA.

RO; GO:0006810; P:transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 RACRIKKKAQYEANKVKIMGINTEYDNILI-FVINSIKQEIVNRVQNPRDERGPN--MGQK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S., Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1016 AA; 111684 MW; CA8958E385587E0B CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZg46900513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%; Score 85; DB 2;
30.9%; Pred. No. 30;
tive 19; Mismatches 2:
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GO; GO:0016020; C:symaptic vesicle; IEA.
GO; GO:0008021; F:transporter activity; IEA.
GO; GO:000810; P:transporter activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :: | : : | :: | Sec IQITVGETMLMGLASATGVYL 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 LEILIKDTLGLPVAGQTSEFV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50004; C2_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM00239; C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pongo pygmaeus (Orangutan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSRDC8 PONPY PRELIMINARY;
QSRDC8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00168; C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9600;
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NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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QSRDC8
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STRAIN-PCC 7421;
MEDLINE-22977040; PubMed=14621292;
MEDLINE-22977040; PubMed=14621292;
Makamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of Gloeobacter violaceus PCC 7421, a
cyanobacterium that lacks thylakoids.";
DNA Res. 10:137-145(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gloeobacter violaceus.
Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacterales; Gloeobacter
                                                                                                                                                                                                                                  Gaps
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R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016524; F:ATP binding; IEA.

GO; GO:001651; F:Kinase activity; IEA.

GO; GO:000155; F:two-component sensor molecule activity; IEA.

GO; GO:000165; F:two-component signal transduction; IEA.

GO; GO:0000160; P:two-component signal transduction system (p. ..;

R InterPro; IPR003594; ATPbind ATPase.

R InterPro; IPR003661; His Kinase.

R InterPro; IPR003661; His Kinase.

R InterPro; IPR003661; His Kinase.

R InterPro; IPR004368; His Kinalam.

R InterPro; IPR004368; His Kinalam.

R InterPro; IPR00014; PAS.

R InterPro; IPR000700; PAS-assoc_C.

R Pfam; PF00672; HAMP; 1.

R Pfam; PF00612; HisRA; I.

R Pfam; PF00612; HisRA; I.

R Pfam; PF00512; HisRA; I.

R Pfam; PF00512; HisRA; I.
                                                                                                                                                                                                                                  22;
                                                                                                                                                                                           15.2%; Score 84; DB 2; Length 1000; 29.7%; Pred. No. 36;
InterPro; IPR000008; C2.
InterPro; IPR001565; Synaptotagmin.
Pfam; PP00168; C2.
Prints; PR00336; C2D0MAIN.
PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM00239; C2; 1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
Hypothetical protein.
SEQUENCE 1000 AA; 110365 MW; FB307C795DA63C92 CRC64;
                                                                                                                                                                                                                                31; Indels
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SEQUENCE 718 AA; 78094 MW; D3E695454C0956DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                      567 QITVGENMLMGLASATGVYLAAL-----PTPG--GIQI 597
                                                                                                                                                                                                                                                                                                                                                63 EILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Two-component sensor histidine Kinase.
OrderedLocusNames=g110814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    718 AA
                                                                                                                                                                                                                                18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00344; BCTRLSENSOR.
TIGRRAMs; TIGR00229; sensory_box; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50113; PAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                              Best Local Similarity 29.74
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7NMF2_GLOVI PRELIMINARY;
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                                                                                                                                                                                               Query Match
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15.0%; Score 82.5; DB 2; Length 718; 24.3%; Pred. No. 35;

Query Match Best Local Similarity

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                                          46
                        3 AFRACRIKKKAQYEANKVKIMGINTEYDNILFVINSIKOEIV------NR----
47; Gaps
45; Indels
                                                                              47 VONPRDERGPNMGOKLEILIKDTLGLPVAGOTSEFVNQVLE----
 20; Mismatches
                                                                                                                                88 -----KTAEGNPTGGLVGLRIPTSK 107
                                                                                                                                                           461 LOITAAPLRTGEGELLGGVAVLRDITAQ 488
                                                                                                                                                                                                Search completed: February 28, 2006, 08:53:06 Job time : 41.609 secs
 36; Conservative
  Matches
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